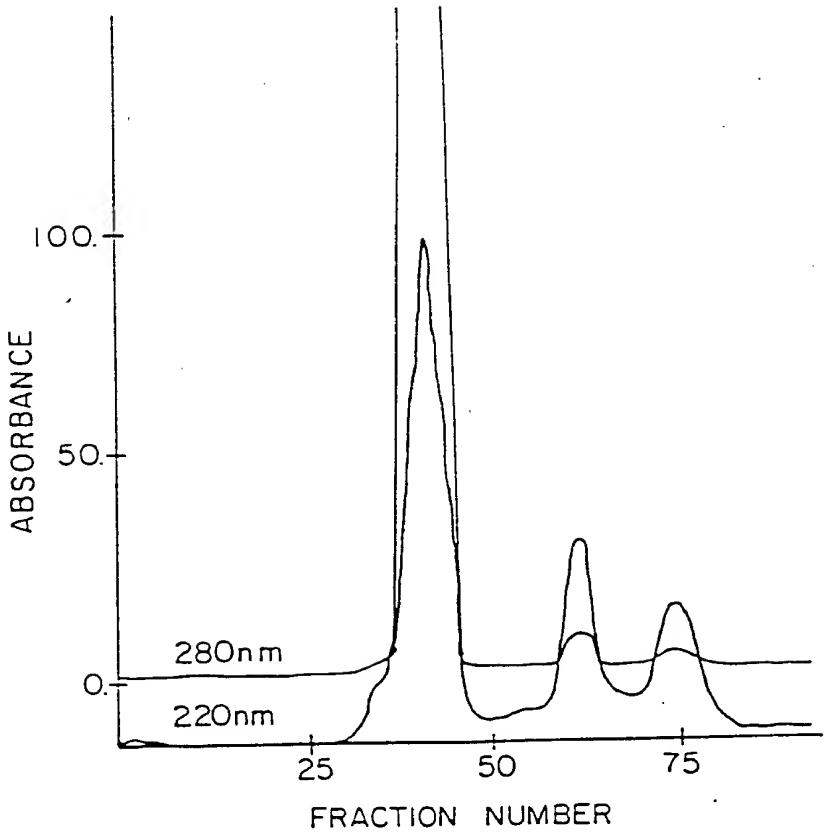

100.
50.
0.
ABSORBANCE
280nm
220nm
25
50
75
FRACTION NUMBER

Fig. 1a

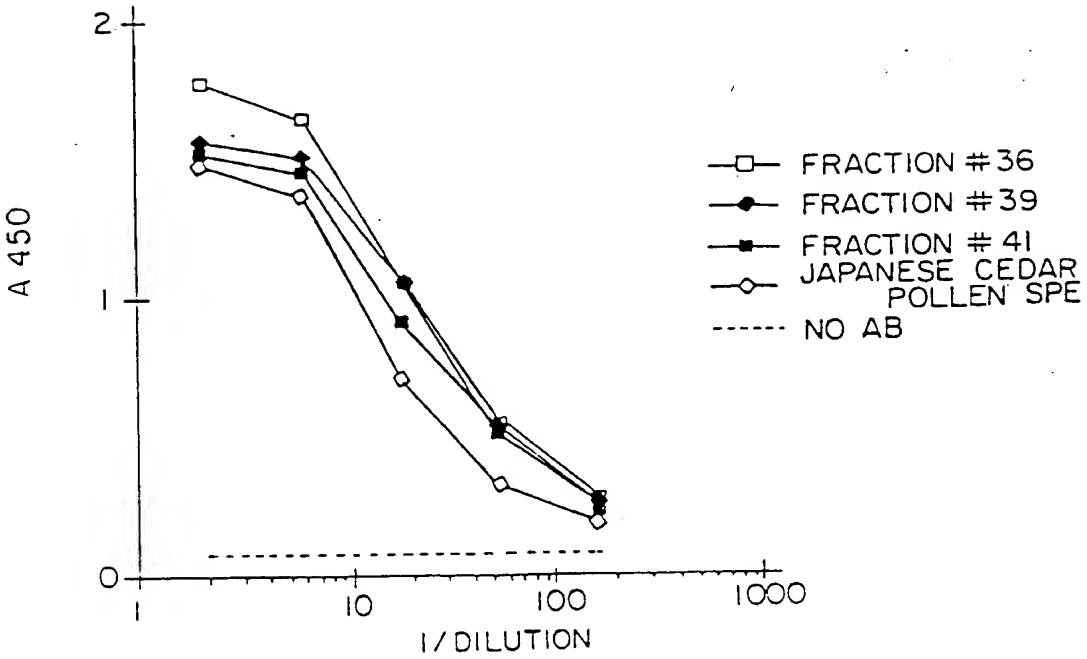

2
1
0
A 450
1
10
100
1000
1/DILUTION
FRACTION #36
FRACTION #39
FRACTION #41
JAPANESE CEDAR POLLEN SPE
NO AB

Fig. 3

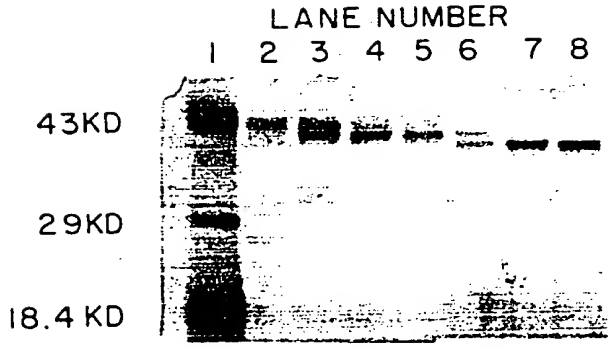


Fig. 1b

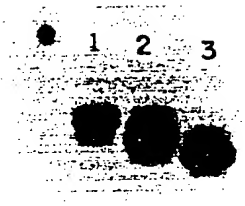


Fig. 2

```
5'-AGTCAATCTG CTCATAATCA TAGCATAGCC GTATAGAAAG AAATTCTACA CTCTGCTACC    60

AAAAA ATG GAT TCC CCT TGC TTA GTA GCA TTA CTG GTT TTC TCT TTT          107
      Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe
      -21 -20                 -15                 -10

GTA ATT GGA TCT TGC TTT TCT GAT AAT CCC ATA GAC AGC TGC TGG AGA        155
Val Ile Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg
         -5                  1                   5

GGA GAC TCA AAC TGG GCC CAA AAT AGA ATG AAG CTC GCA GAT TGT GCA        203
Gly Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala
 10                  15                  20                  25

GTG GGC TTC GGA AGC TCC ACC ATG GGA GGC AAG GGA GGA GAT CTT TAT        251
Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr
                 30                  35                  40

ACG GTC ACG AAC TCA GAT GAC GAC CCT GTG AAT CCT GCA CCA GGA ACT        299
Thr Val Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr
             45                  50                  55

CTG CGC TAT GGA GCA ACC CGA GAT AGG CCC CTG TGG ATA ATT TTC AGT        347
Leu Arg Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser
         60                  65                  70
```

Fig. 4

```
GGG AAT ATG AAT ATA AAG CTC AAA ATG CCT ATG TAC ATT GCT GGG TAT      395
Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr
     75                  80                  85

AAG ACT TTT GAT GGC AGG GGA GCA CAA GTT TAT ATT GGC AAT GGC GGT      443
Lys Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly
 90                  95                 100                 105

CCC TGT GTG TTT ATC AAG AGA GTT AGC AAT GTT ATC ATA CAC GGT TTG      491
Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu
                110                 115                 120

TAT CTG TAC GGC TGT AGT ACT AGT GTT TTG GGG AAT GTT TTG ATA AAC      539
Tyr Leu Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn
            125                 130                 135

GAG AGT TTT GGG GTG GAG CCT GTT CAT CCT CAG GAT GGC GAT GCT CTT      587
Glu Ser Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu
        140                 145                 150

ACT CTG CGC ACT GCT ACA AAT ATT TGG ATT GAT CAT AAT TCT TTC TCC      635
Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser
    155                 160                 165
```

Fig. 4 cont.

```
AAT TCT TCT GAT GGT CTG GTC GAT GTC ACT CTT ACT TCG ACT GGA GTT      683
Asn Ser Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val
170                 175                 180                 185

ACT ATT TCA AAC AAT CTT TTT TTC AAC CAT CAT AAA GTG ATG TTG TTA      731
Thr Ile Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu
                190                 195                 200

GGG CAT GAT GAT GCA TAT AGT GAT GAC AAA TCC ATG AAG GTG ACA GTG      779
Gly His Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val
            205                 210                 215

GCG TTC AAT CAA TTT GGA CCT AAC TGT GGA CAA AGA ATG CCC AGG GCA      827
Ala Phe Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala
        220                 225                 230

CGA TAT GGA CTT GTA CAT GTT GCA AAC AAT AAT TAT GAC CCA TGG ACT      875
Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr
    235                 240                 245

ATA TAT GCA ATT GGT GGG AGT TCA AAT CCA ACC ATT CTA AGT GAA GGG      923
Ile Tyr Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly
250                 255                 260                 265
```

Fig. 4 cont.

```
AAT AGT TTC ACT GCA CCA AAT GAG AGC TAC AAG AAG CAA GTA ACC ATA          971
Asn Ser Phe Thr Ala Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile
                270                 275                 280

CGT ATT GGA TGC AAA ACA TCA TCA TCT TGT TCA AAT TGG GTG TGG CAA         1019
Arg Ile Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp Gln
            285                 290                 295

TCT ACA CAA GAT GTT TTT TAT AAT GGA GCT TAT TTT GTA TCA TCA GGG         1067
Ser Thr Gln Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly
        300                 305                 310

AAA TAT GAA GGG GGT AAT ATA TAC ACA AAG AAA GAA GCT TTC AAT GTT         1115
Lys Tyr Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val
    315 320 325

GAG AAT GGG AAT GCA ACT CCT CAA TTG ACA AAA AAT GCT GGG GTT TTA         1163
Glu Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys Asn Ala Gly Val Leu
330                 335                 340                 345

ACA TGC TCT CTC TCT AAA CGT TGT TGATGATGCA TATATTCTAG CATGTTGTAC        1217
Thr Cys Ser Leu Ser Lys Arg Cys
                350

TATCTAAATT AACATCAACA AGAAAATATA TCATGATGTA TATTGTTGTA TTGATGTCAA       1277

AATAAAAATG TATCTTTTAC TATTAAAAAA AAAAATGATC GATCGGACGG TACCTCTAGA-3'    1337
```

Fig. 4 cont.

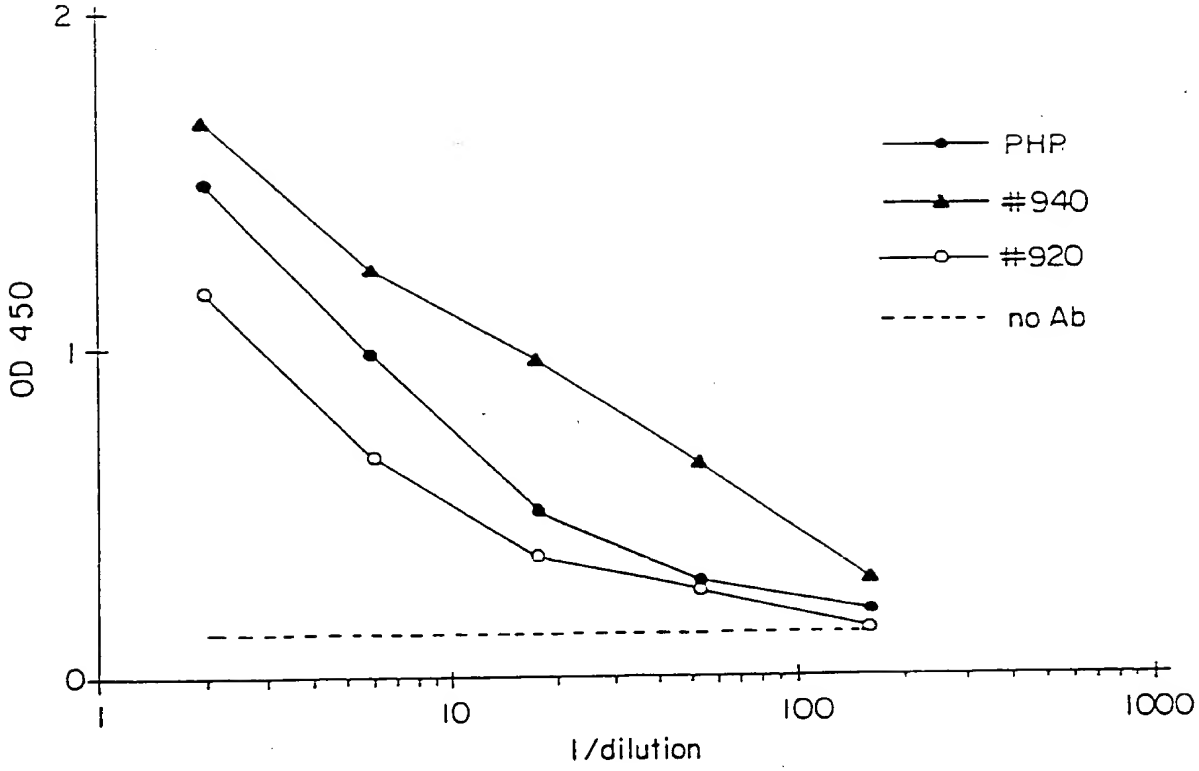

2
1
0
OD 450
1
10
100
1000
1/dilution
PHP
#940
#920
no Ab

Fig. 5a

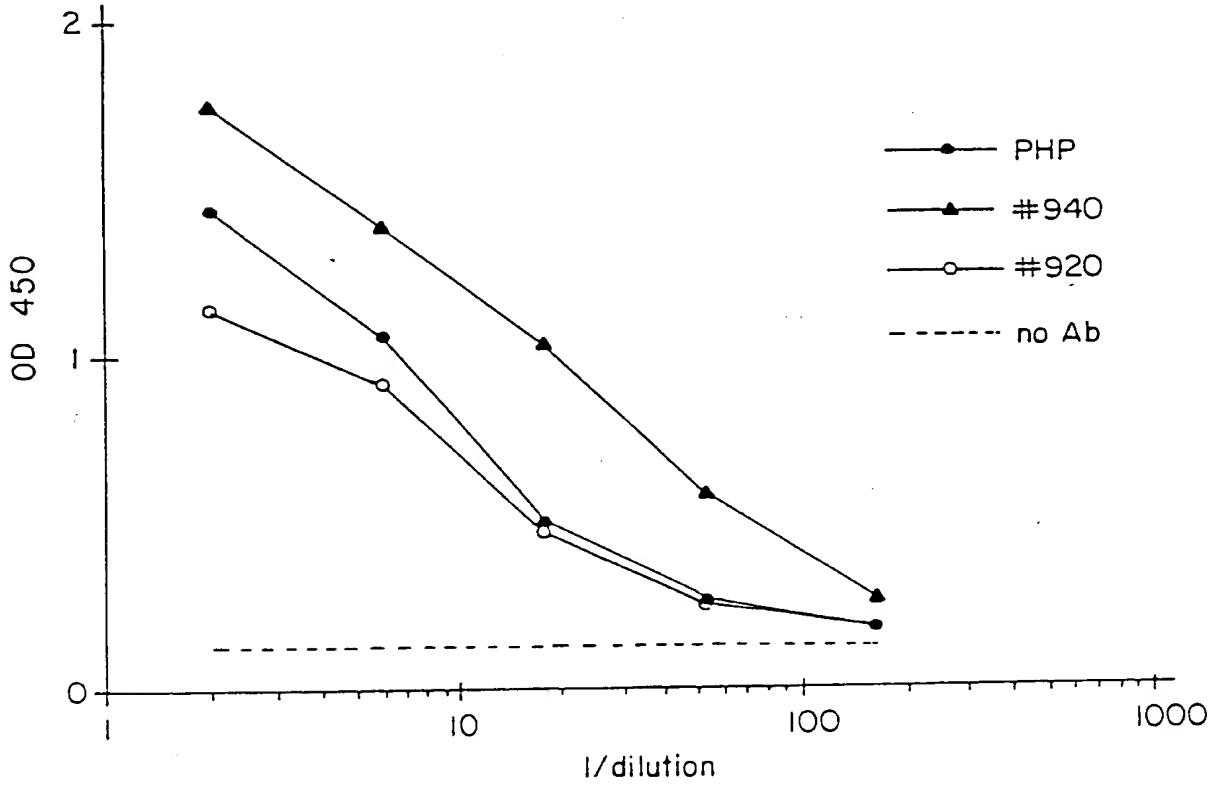

2
1
0
OD 450
1
10
100
1000
1/dilution
PHP
#940
#920
no Ab

Fig. 5b

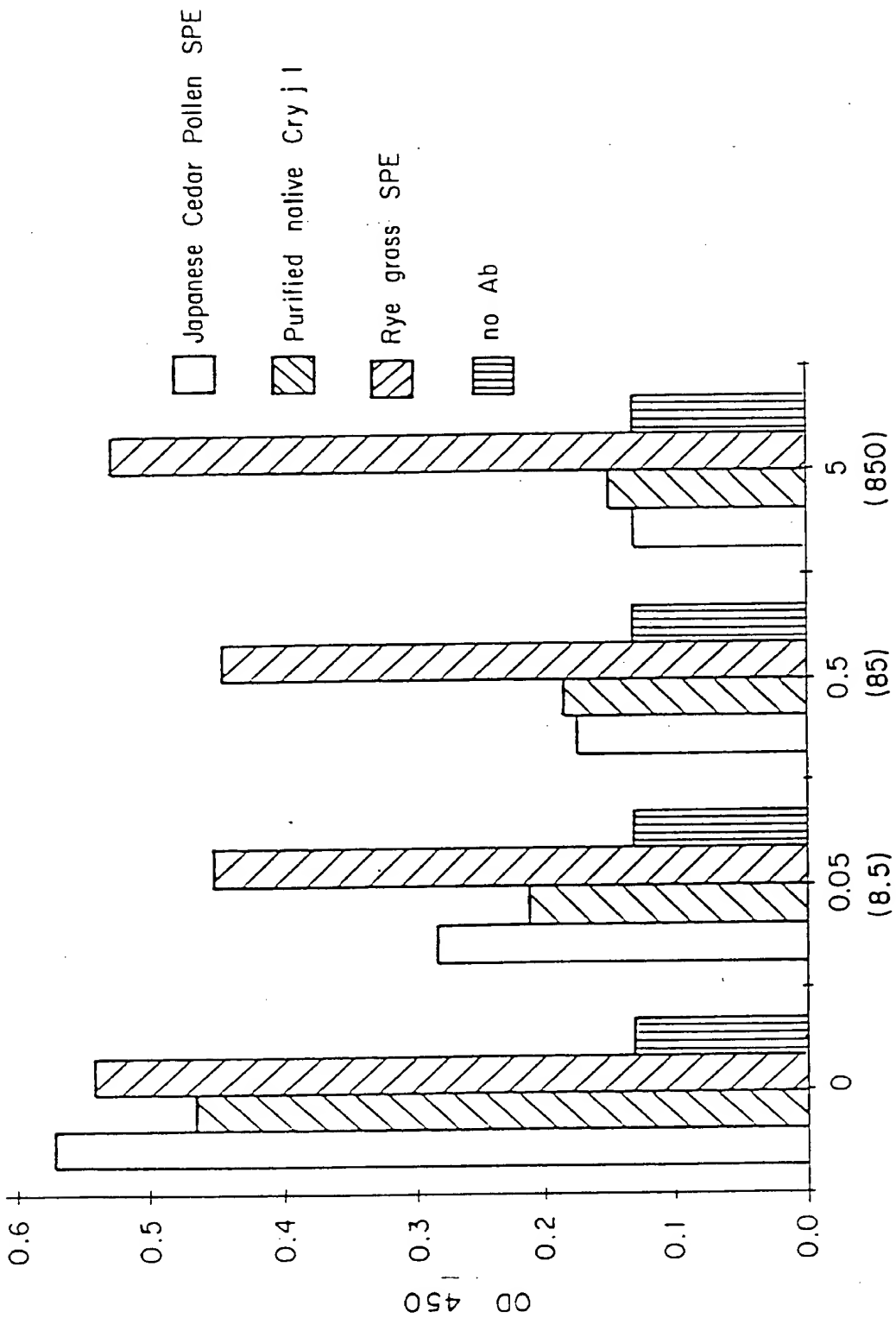

Japanese Cedar Pollen SPE
Purified nolive Cry j I
Rye grass SPE
no Ab
OD 450
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0
0.05 (8.5)
0.5 (85)
5 (850)
concentration of protein In ug/ml

Fig. 6

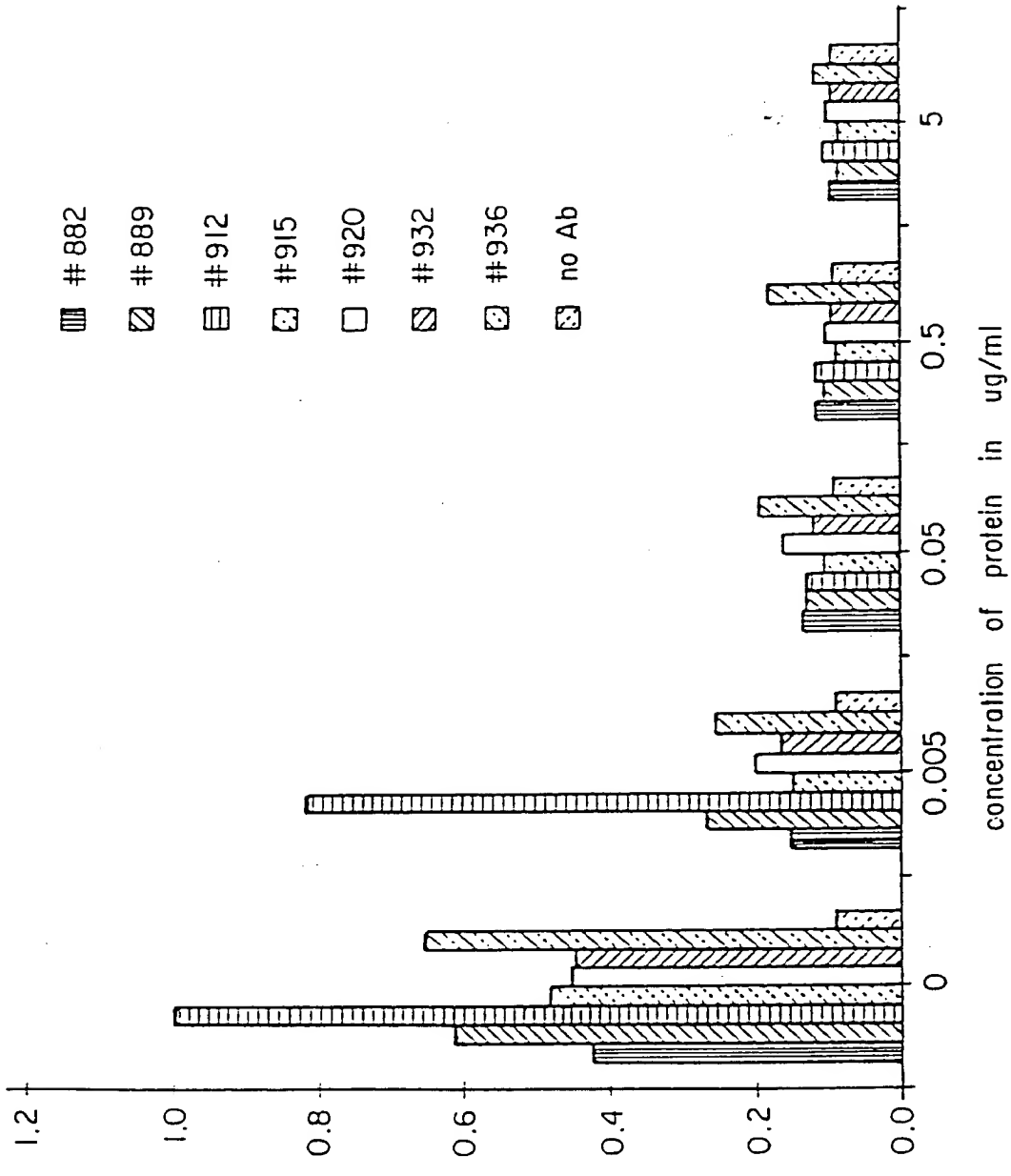
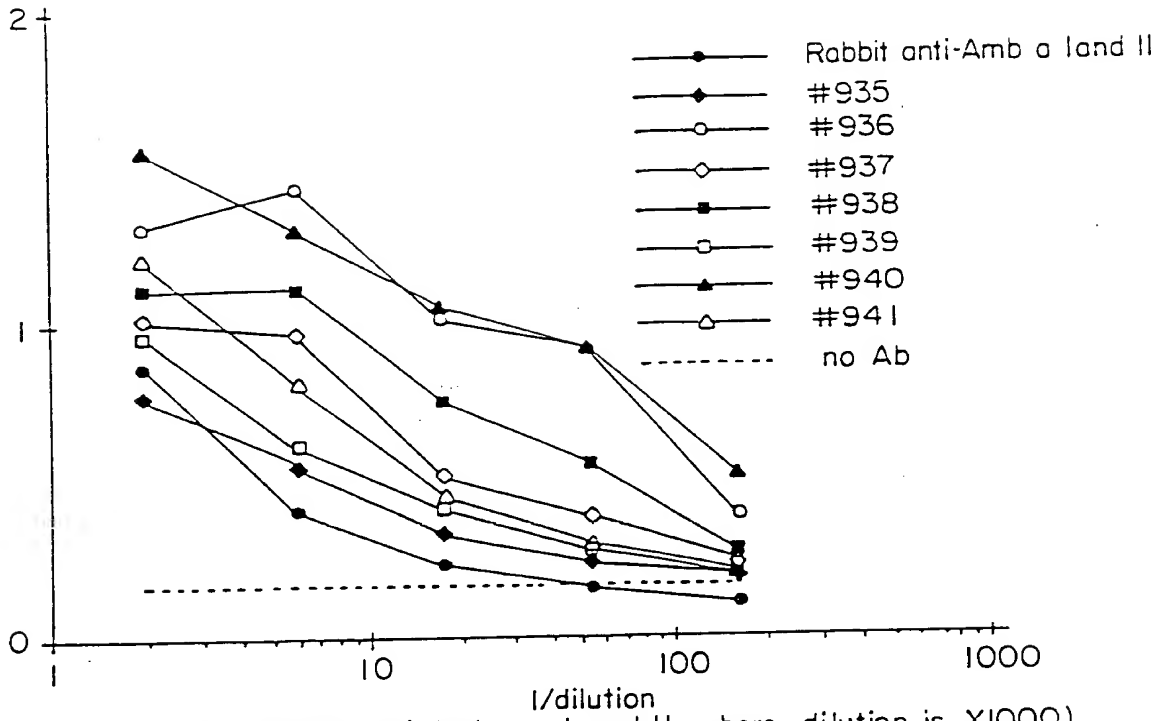
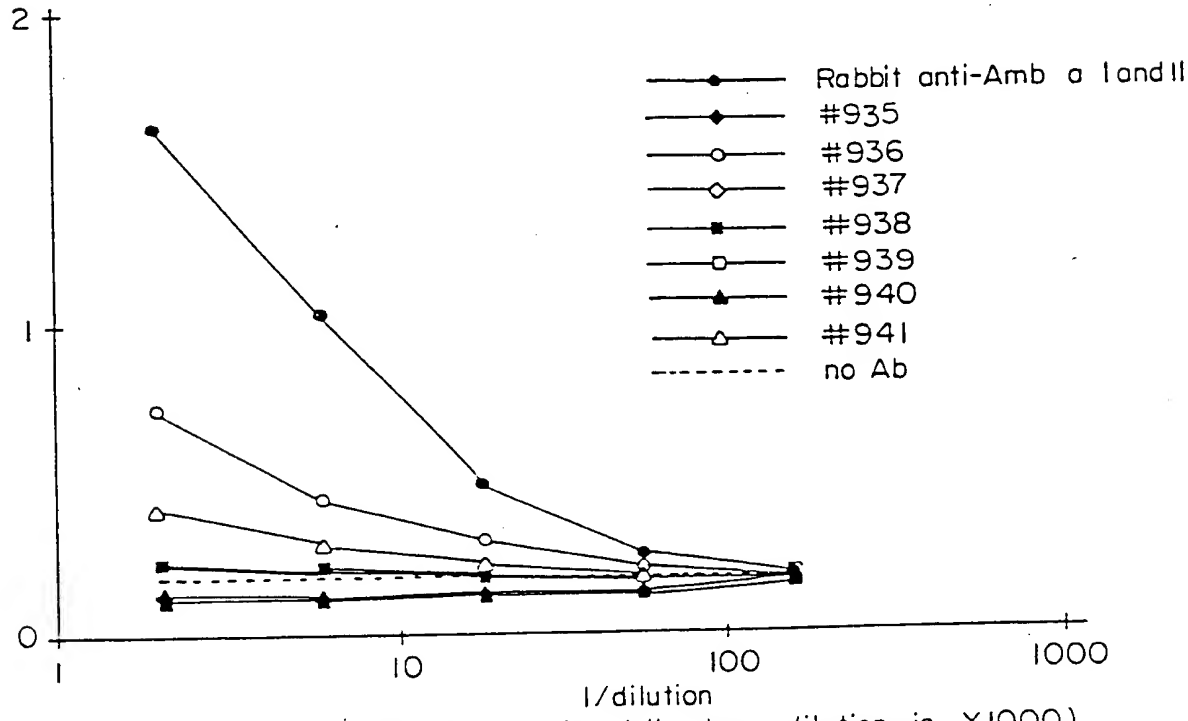

#882
#889
#912
#915
#920
#932
#936
no Ab
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
0.005
0.05
0.5
5
concentration of protein in ug/ml

Fig. 7



(Except for Rabbit anti-Amb a I and II, where dilution is X1000)

Fig. 8a



(Except for Rabbit anti-Amb a I and II, where dilution is X1000)

Fig. 8b

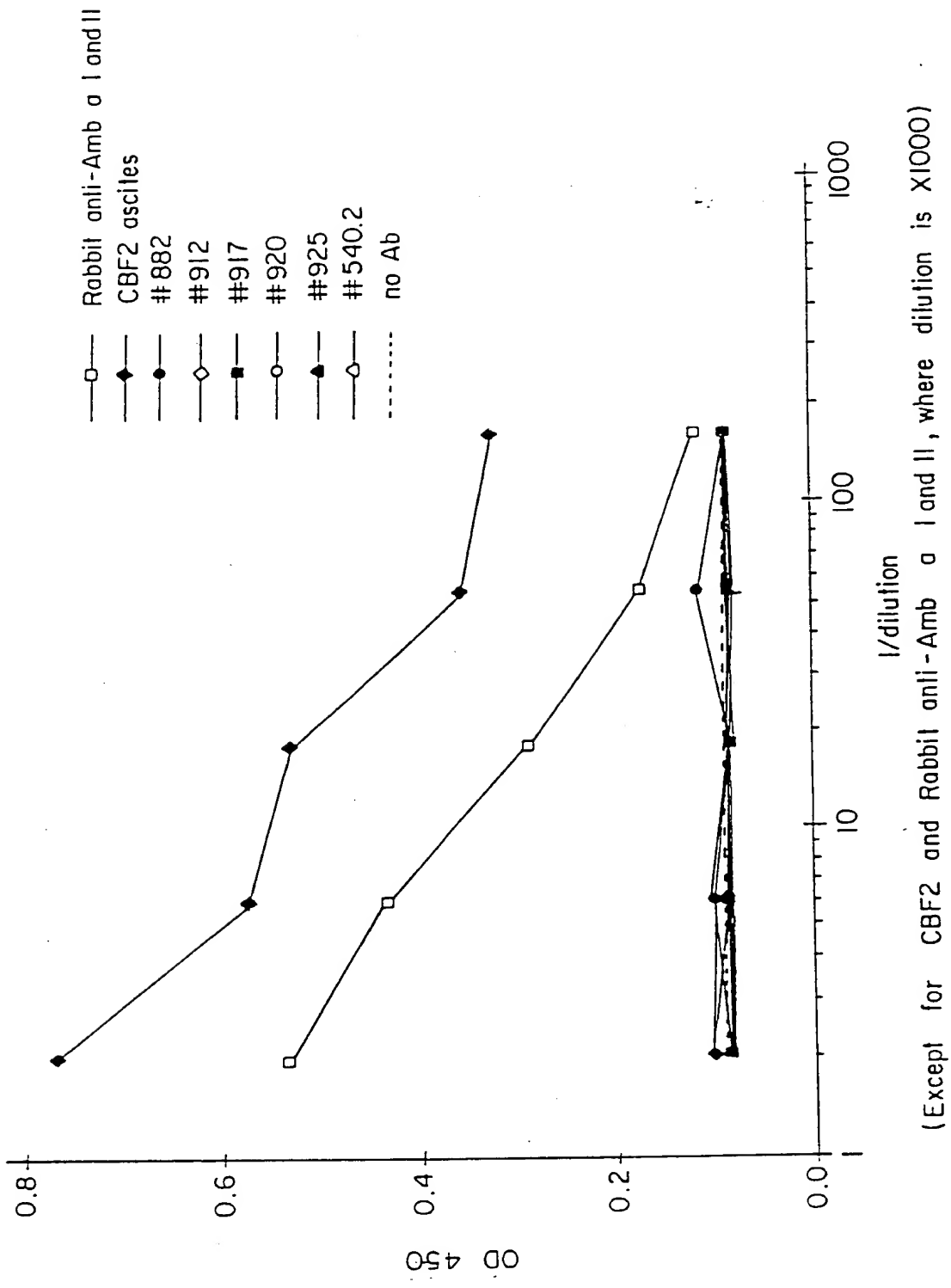

Rabbit anti-Amb a I and II
CBF2 ascites
#882
#912
#917
#920
#925
#540.2
no Ab
OD 450
0.8
0.6
0.4
0.2
0.0
1
10
100
1000
1/dilution
(Except for CBF2 and Rabbit anti-Amb a I and II, where dilution is X1000)

Fig. 9

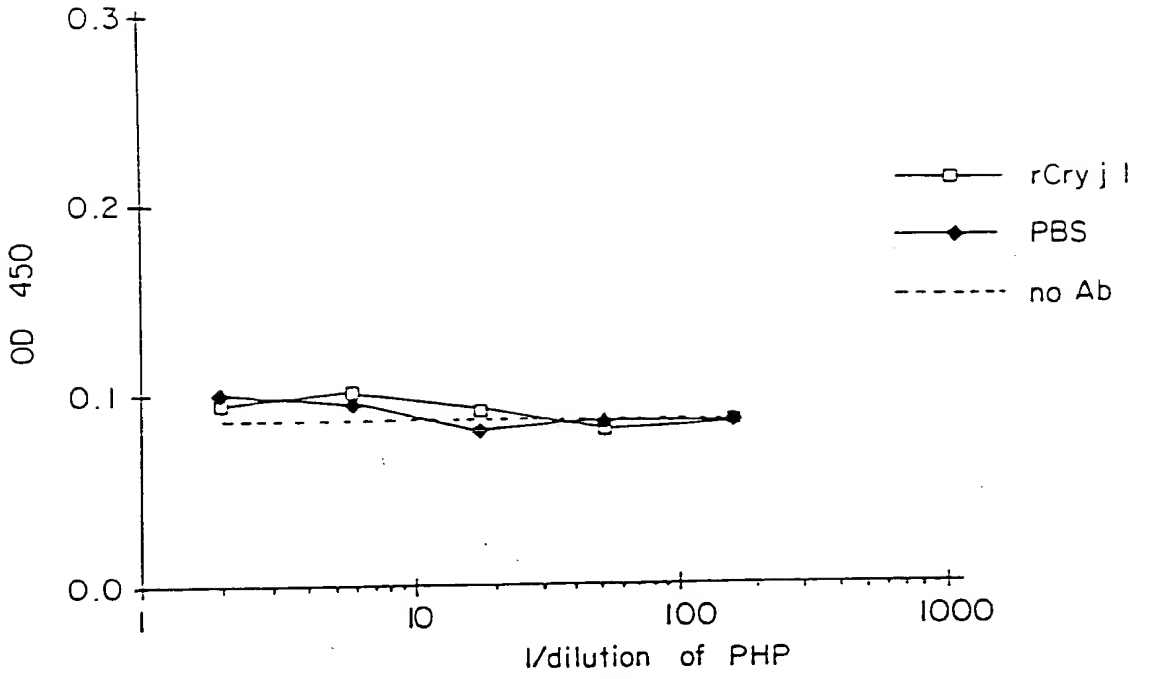


Fig. 10a

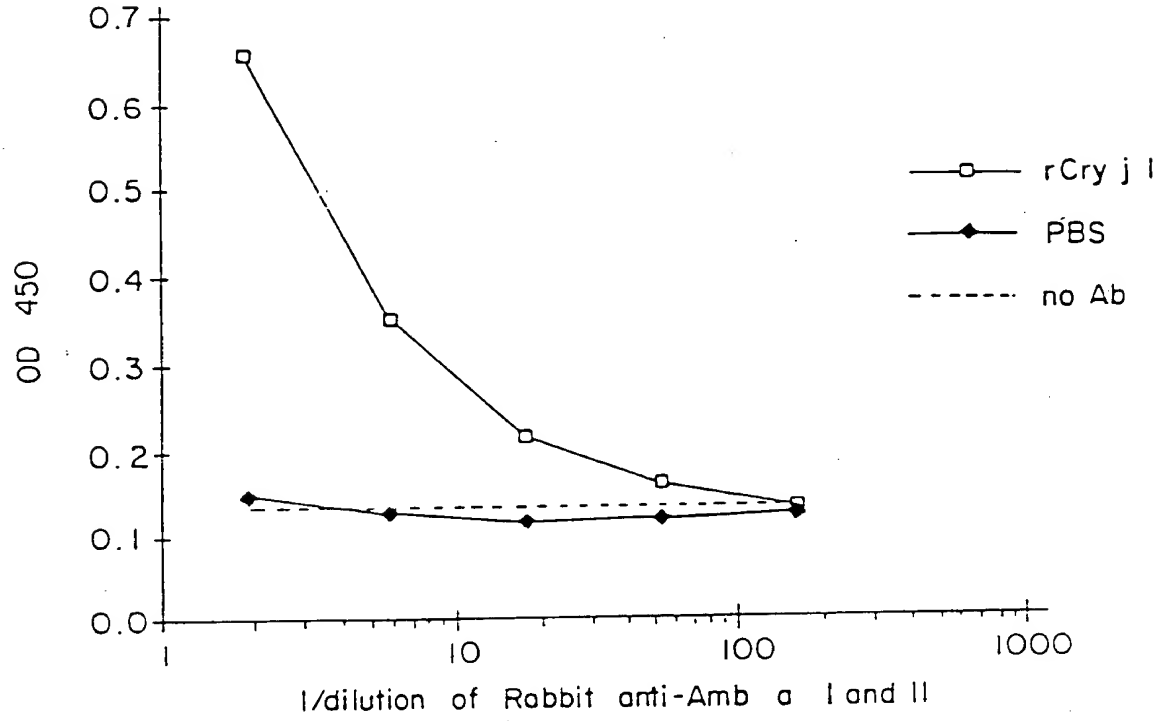


Fig. 10b

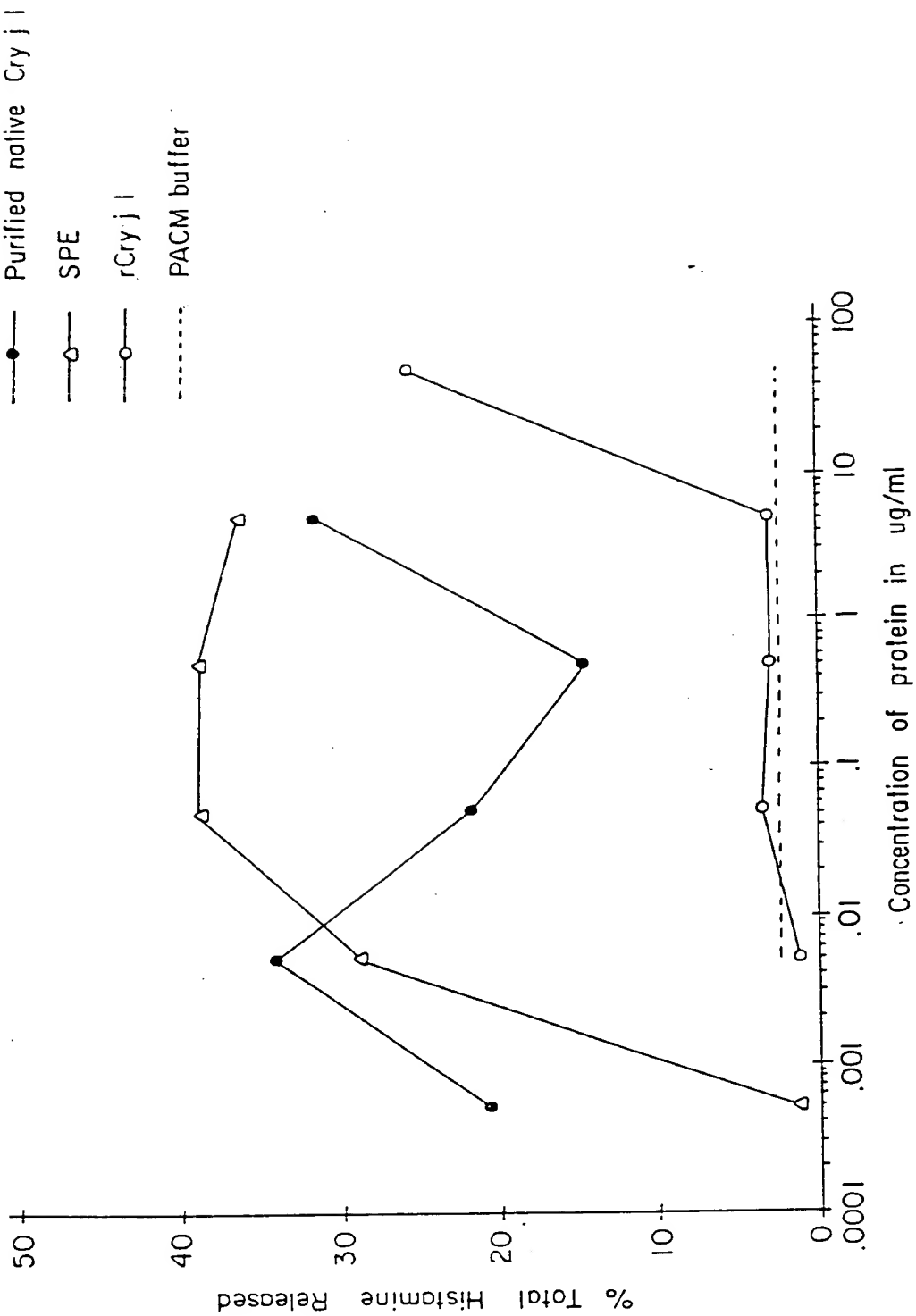

Purified native Cry j I
SPE
rCry j I
PACM buffer
% Total Histamine Released
0
10
20
30
40
50
.0001
.001
.01
.1
1
10
100
Concentration of protein in ug/ml

Fig. 11

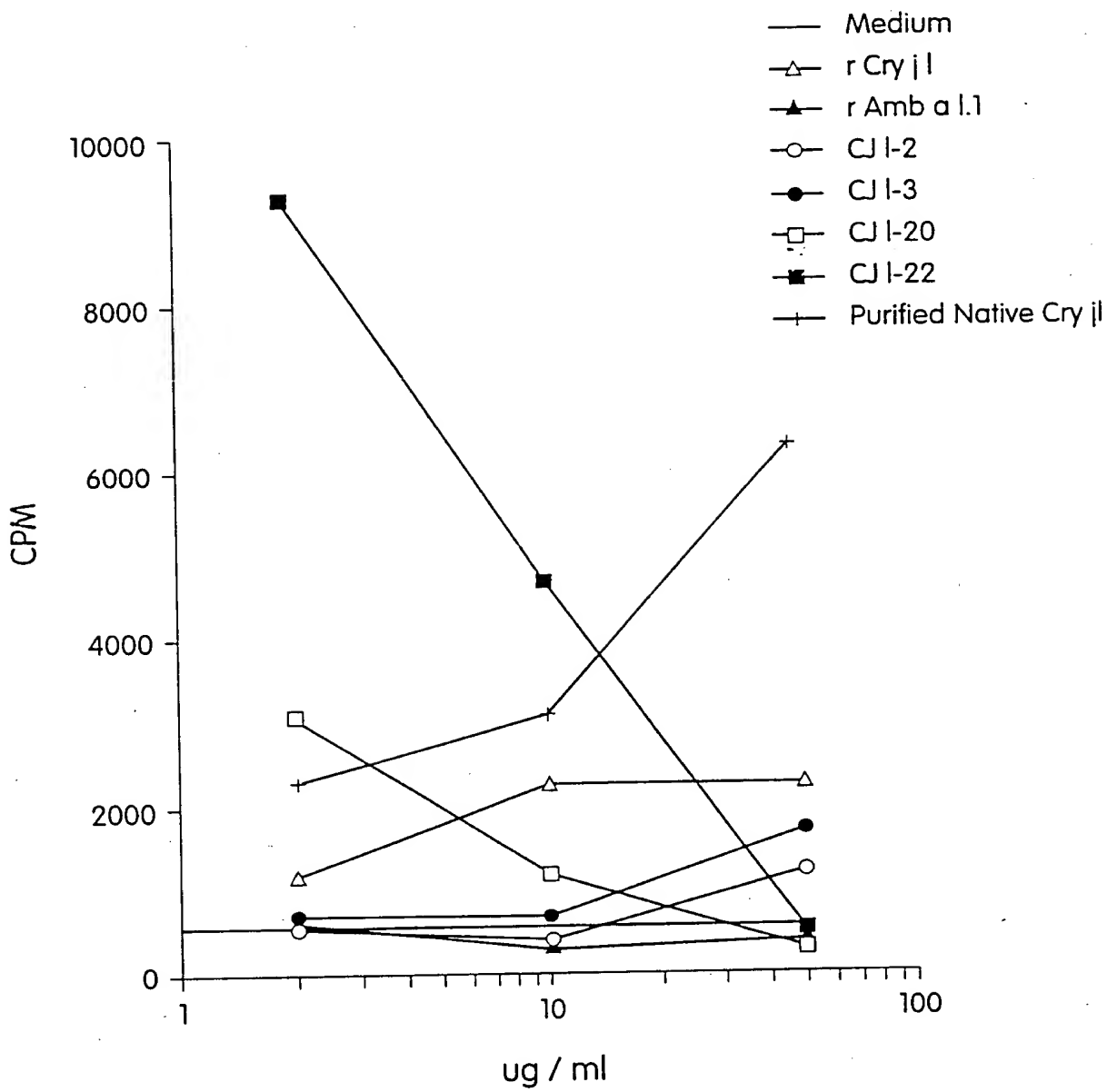

Medium
r Cry j I
r Amb a I.1
CJ I-2
CJ I-3
CJ I-20
CJ I-22
Purified Native Cry jI
10000
8000
6000
4000
2000
0
CPM
1
10
100
ug / ml

Fig. 12

PEPTIDE NAME	
CJI-1 (1-20)	DNPIDSCWRGDSNWAQNRMK
CJI-2 (11-30)	DSNWAQNRMKLADCAVGFGS
CJI-3 (21-40)	LADCAVGFGSSTMGGKGGDL
CJI-4 (31-50)	STMGGKGGDLYTVTNSDDDP
CJI-5 (41-60)	YTVTNSDDDPVNPAPGTLRY
CJI-6 (51-70)	VNPAPGTLRYGATRDRPLWI
CJI-7 (61-80)	GATRDRPLWIIFSGNMNIKL
CJI-8 (71-90)	IFSGNMNIKLKMPMYIAGYK
CJI-9 (81-100)	KMPMYIAGYKTFDGRGAQVY
CJI-10 (91-110)	TFDGRGAQVYIGNGGPCVFI
CJI-11 (101-120)	IGNGGPCVFIKRVSNVIIHG
CJI-12 (111-130)	KRVSNVIIHGLYLYGCSTSV
CJI-13 (121-140)	LYLYGCSTSVLGNVLINESF
CJI-14 (131-150)	LGNVLINESFGVEPVHPQDG
CJI-15 (141-160)	GVEPVHPQDGDALTLRTATN
CJI-16 (151-170)	DALTLRTATNIWIDHNSFSN
CJI-17 (161-180)	IWIDHNSFSNSSDGLVDVTL
CJI-18 (171-190)	SSDGLVDVTLTSTGVTISNN
CJI-19 (181-200)	TSTGVTISNNLFFNHHKVML
CJI-20 (191-210)	LFFNHHKVMLLGHDDAYSDD
CJI-21 (201-220)	LGHDDAYSDDKSMKVTVAFN
CJI-22 (211-230)	KSMKVTVAFNQFGPNCGQRM
CJI-23 (221-240)	QFGPNCGQRMPRARYGLVHV
CJI-24 (231-250)	PRARYGLVHVANNNYDPWTI
CJI-25 (241-260)	ANNNYDPWTIYAIGGSSNPT
CJI-26 (251-270)	YAIGGSSNPTILSEGNSFTA
CJI-27 (261-280)	ILSEGNSFTAPNESYKKQVT
CJI-28 (271-290)	PNESYKKQVTIRIGCKTSSS
CJI-29 (281-300)	IRIGCKTSSSCSNWVWQSTQ
CJI-30 (291-310)	CSNWVWQSTQDVFYNGAYFV
CJI-31 (301-320)	DVFYNGAYFVSSGKYEGGNI
CJI-32 (311-330)	SSGKYEGGNIYTKKEAFNVE
CJI-33 (321-340)	YTKKEAFNVENGNATPQLTK
CJI-34 (331-350)	NGNATPQLTKNAGVLTCSLS
CJI-35 (341-353)	NAGVLTCSLSKRC

Fig. 13

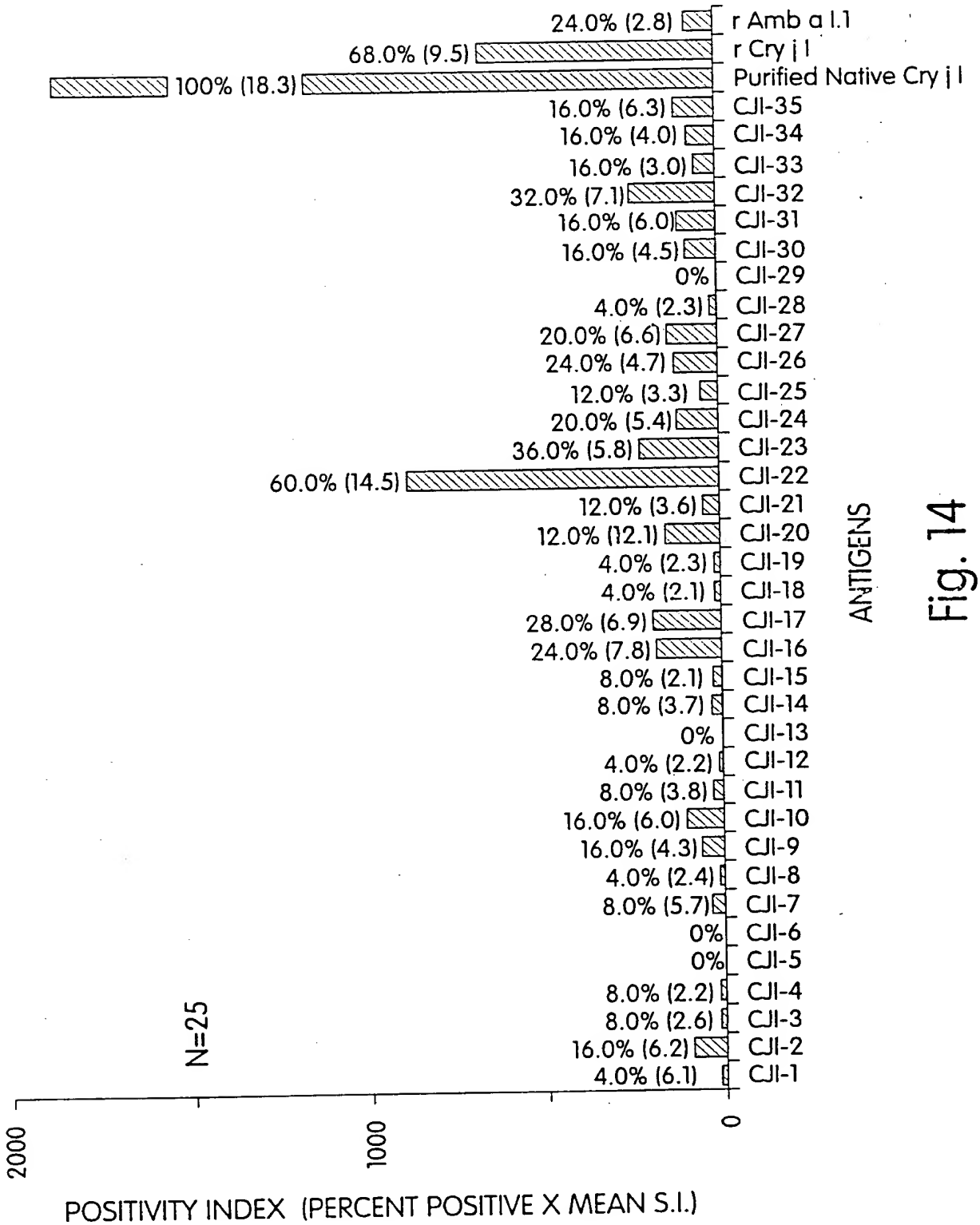

24.0% (2.8)
r Amb a I.1
68.0% (9.5)
r Cry j I
100% (18.3)
Purified Native Cry j I
16.0% (6.3)
CJI-35
16.0% (4.0)
CJI-34
16.0% (3.0)
CJI-33
32.0% (7.1)
CJI-32
16.0% (6.0)
CJI-31
16.0% (4.5)
CJI-30
0%
CJI-29
4.0% (2.3)
CJI-28
20.0% (6.6)
CJI-27
24.0% (4.7)
CJI-26
12.0% (3.3)
CJI-25
20.0% (5.4)
CJI-24
36.0% (5.8)
CJI-23
60.0% (14.5)
CJI-22
12.0% (3.6)
CJI-21
12.0% (12.1)
CJI-20
4.0% (2.3)
CJI-19
4.0% (2.1)
CJI-18
28.0% (6.9)
CJI-17
24.0% (7.8)
CJI-16
8.0% (2.1)
CJI-15
8.0% (3.7)
CJI-14
0%
CJI-13
4.0% (2.2)
CJI-12
8.0% (3.8)
CJI-11
16.0% (6.0)
CJI-10
16.0% (4.3)
CJI-9
4.0% (2.4)
CJI-8
8.0% (5.7)
CJI-7
0%
CJI-6
0%
CJI-5
8.0% (2.2)
CJI-4
8.0% (2.6)
CJI-3
16.0% (6.2)
CJI-2
4.0% (6.1)
CJI-1
N=25
2000
1000
0
POSITIVITY INDEX (PERCENT POSITIVE X MEAN S.I.)
ANTIGENS

Fig. 14

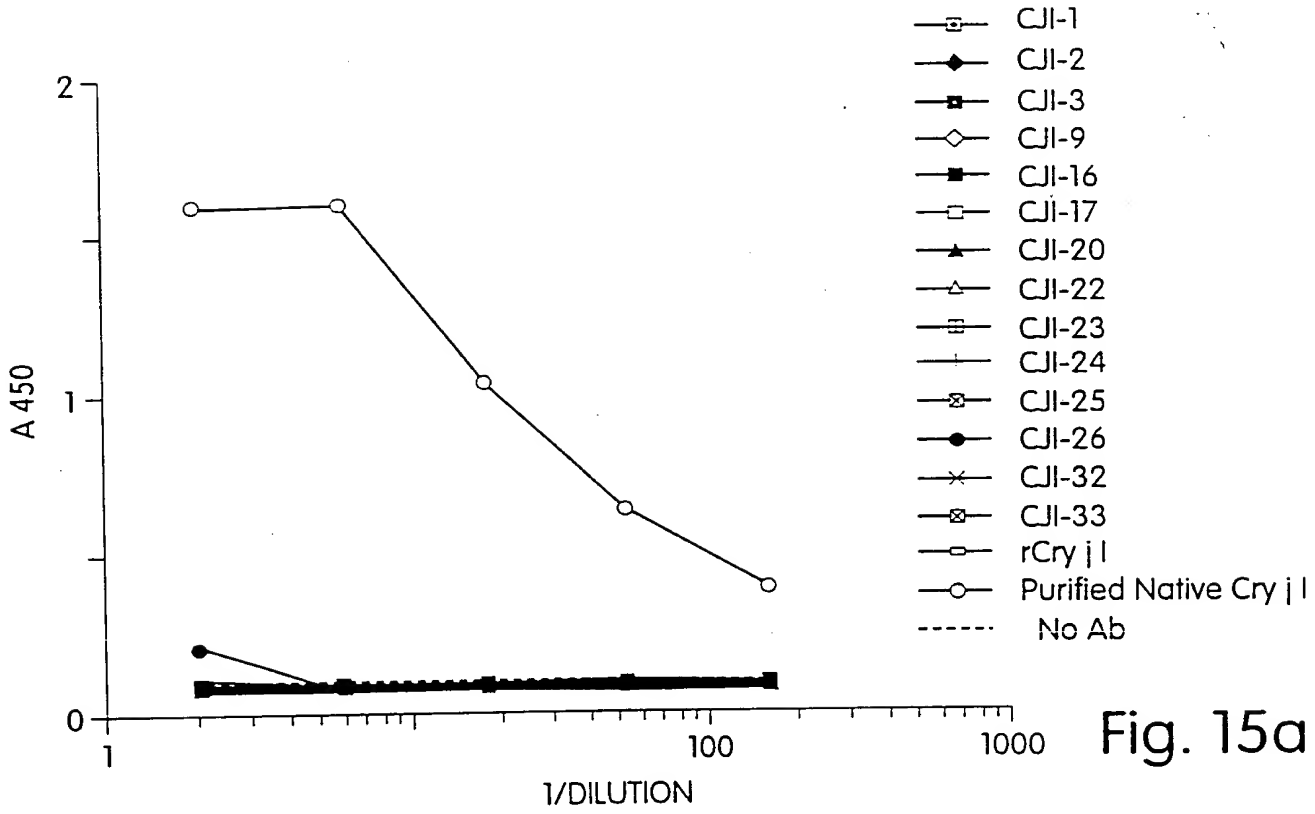


Fig. 15a

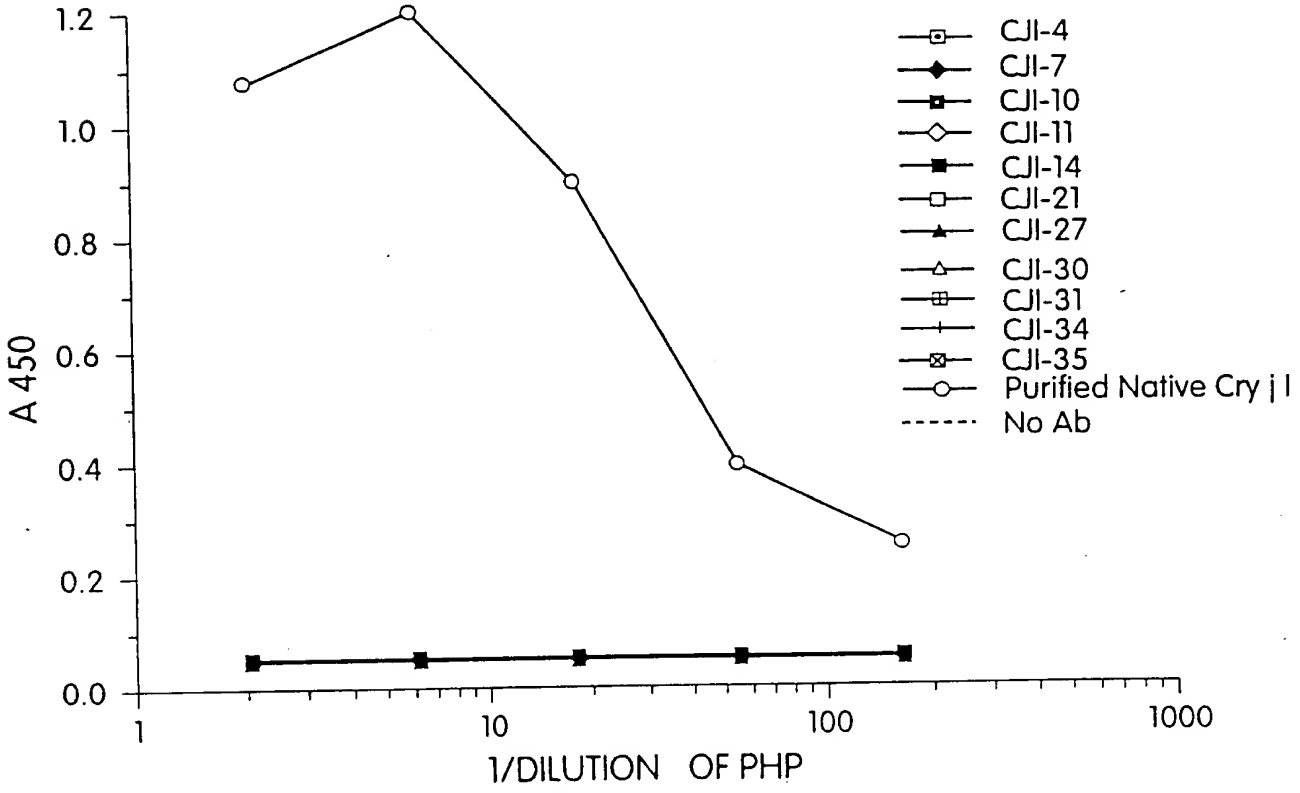


Fig. 15b

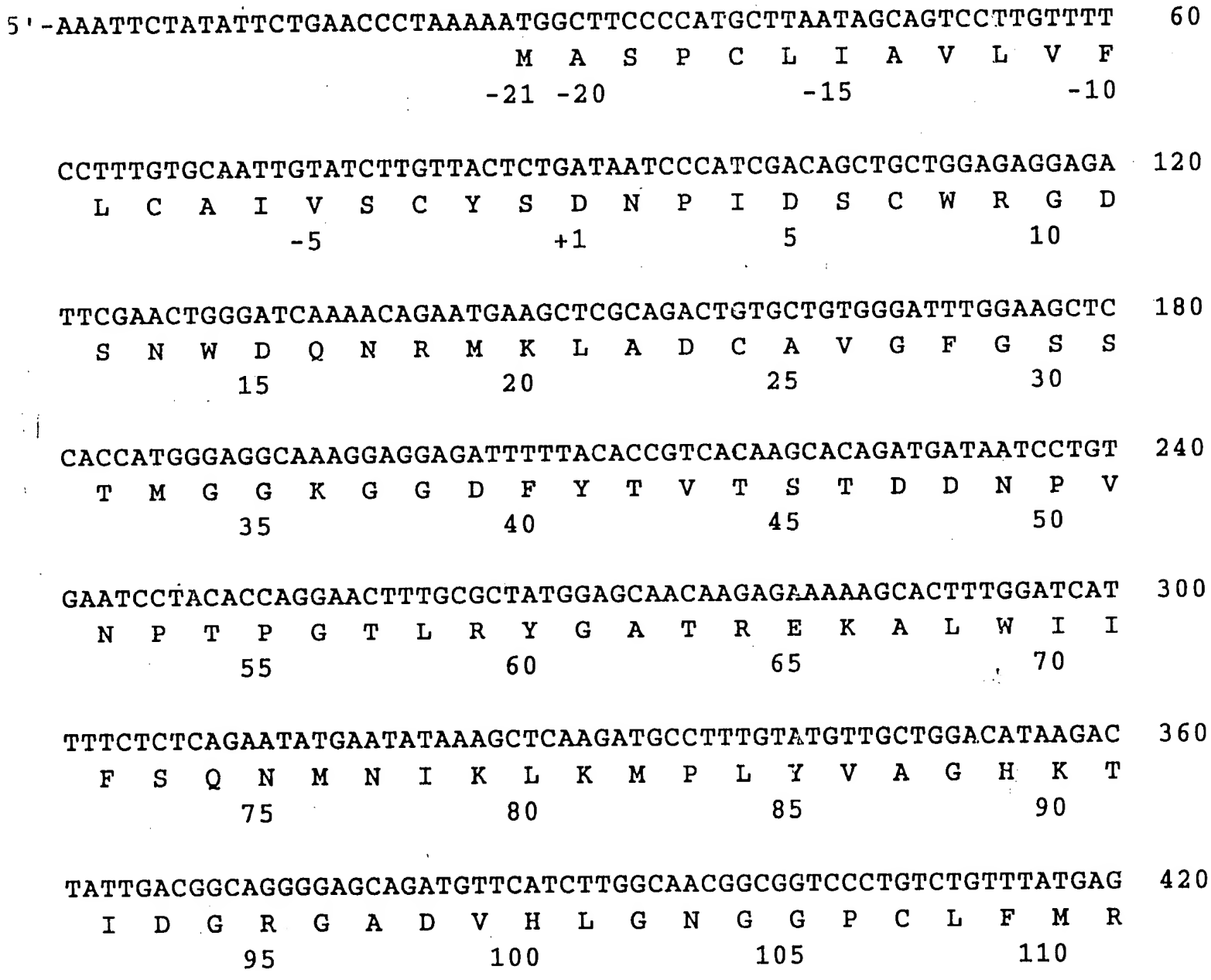


Fig. 16

```
GAAAGTGAGCCATGTTATTCTCCATAGTTTGCATATACACGGTTGTAATACGAGTGTTTT   480
  K  V  S  H  V  I  L  H  S  L  H  I  H  G  C  N  T  S  V  L
        115            120            125            130

GGGGGATGTTTTGGTAAGTGAGTCTATTGGGGTCGAGCCTGTTCATGCTCAGGATGGGGA   540
  G  D  V  L  V  S  E  S  I  G  V  E  P  V  H  A  Q  D  G  D
        135            140            145            150

CGCCATTACTATGCGCCATGTTACAAATGCTTGGATTGATCATAATTCTCTCTCCGATTG   600
  A  I  T  M  R  H  V  T  N  A  W  I  D  H  N  S  L  S  D  C
        155            160            165            170

TTCTGATGGTCTTATCGATGTTACGCTTGGCTCCACTGGAATTACTATCTCCAACAATCA   660
  S  D  G  L  I  D  V  T  L  G  S  T  G  I  T  I  S  N  N  H
        175            180            185            190

CTTCTTCAACCATCATAAAGTGATGTTATTAGGACATGATGATACATATGACGATGACAA   720
  F  F  N  H  H  K  V  M  L  L  G  H  D  D  T  Y  D  D  D  K
        195            200            205            210

ATCTATGAAAGTGACAGTGGCGTTCAATCAATTTGGACCTAATGCTGGGCAAAGAATGCC   780
  S  M  K  V  T  V  A  F  N  Q  F  G  P  N  A  G  Q  R  M  P
        215            220            225            230
```

Fig. 16 cont.

08/226248

```
AAGGGCACGATATGGACTTGTACATGTTGCAAACAATAATTATGATCCATGGAATATATA  840
  R  A  R  Y  G  L  V  H  V  A  N  N  N  Y  D  P  W  N  I  Y
           235               240               245               250

TGCTATTGGTGGGAGTTCAAATCCAACCATTCTGAGTGAAGGGAATAGTTTCACTGCCCC  900
  A  I  G  G  S  S  N  P  T  I  L  S  E  G  N  S  F  T  A  P
           255               260               265               270

AAGTGAGAGTTACAAGAAGCAAGTAACAAAGCGTATAGGGTGTGAATCACCATCAGCTTG  960
  S  E  S  Y  K  K  Q  V  T  K  R  I  G  C  E  S  P  S  A  C
           275               280               285               290

TGCGAACTGGGTGTGGAGATCTACACGAGATGCTTTTATTAATGGAGCTTATTTTGTATC 1020
  A  N  W  V  W  R  S  T  R  D  A  F  I  N  G  A  Y  F  V  S
           295               300               305               310

ATCGGGGAAAACTGAAGAGACCAATATATACAATAGTAATGAAGCTTTCAAAGTTGAGAA 1080
  S  G  K  T  E  E  T  N  I  Y  N  S  N  E  A  F  K  V  E  N
           315               320               325               330

TGGGAATGCAGCTCCTCAATTAACCAAAAATGCTGGAGTTGTAACCTAAGCTCTCTCTAA 1140
  G  N  A  A  P  Q  L  T  K  N  A  G  V  V  T  -
           335               340               345

ATCTTGCTTATGAAACGAAAAAATATATAG-3'                             1170
```

Fig. 16 cont.

```
'-CGGTATAGATAGATTCTATATTCTGAGCCCTAAAAATGGCTTCCCCATGCTTAATAGCAT    60
                                        M  A  S  P  C  L  I  A
                                      -21 -20           -15

TCCTTGTTTTCCTTTGTGCAATTGTATCTTGTTGCTCTGATAATCCCATAGACAGCTGCT    120
F  L  V  F  L  C  A  I  V  S  C  C  S  D  N  P  I  D  S  C
      -10            -5             +1             5

GGAGAGGAGATTCGAACTGGGGTCAAAACAGAATGAAGCTCGCAGATTGCGCTGTGGGAT    180
W  R  G  D  S  N  W  G  Q  N  R  M  K  L  A  D  C  A  V  G
   10             15             20             25

TTGGAAGCTCCACCATGGGAGGCAAAGGAGGAGATTTTTACACCGTCACAAGCGCAGATG    240
F  G  S  S  T  M  G  G  K  G  G  D  F  Y  T  V  T  S  A  D
   30             35             40             45

ATAATCCTGTGAATCCTACACCAGGAACTTTGCGCTATGGAGCAACAAGAGAAAAAGCAC    300
D  N  P  V  N  P  T  P  G  T  L  R  Y  G  A  T  R  E  K  A
   50             55             60             65

TTTGGATCATTTTCTCTCAGAATATGAATATAAAGCTCAAGATGCCTTTGTATGTTGCTG    360
L  W  I  I  F  S  Q  N  M  N  I  K  L  K  M  P  L  Y  V  A
   70             75             80             85

GACATAAGACTATTGACGGCAGGGGAGCAGATGTTCATCTTGGCAACGGCGGTCCCTGTC    420
G  H  K  T  I  D  G  R  G  A  D  V  H  L  G  N  G  G  P  C
   90             95            100            105
```

Fig. 17

08/226248

```
TGTTTATGAGGAAAGTGAGCCATGTTATTCTCCATGGTTTGCATATACACGGTTGTAATA    480
L  F  M  R  K  V  S  H  V  I  L  H  G  L  H  I  H  G  C  N
   110            115            120            125

CTAGTGTTTTGGGGGATGTTTTGGTAAGTGAGTCTATTGGGGTGGTGCCTGTACACCCCC    540
T  S  V  L  G  D  V  L  V  S  E  S  I  G  V  V  P  V  H  P
   130            135            140            145

AGGACGGAGATGCGTTTACTGTGAGGACCTCTGAACATATTTGGGTCGACCATAATACTC    600
Q  D  G  D  A  F  T  V  R  T  S  E  H  I  W  V  D  H  N  T
   150            155            160            165

TCTCCAATGGCACCGACGGCCTCGTCGACGTTACTCTTGCTTCCACTGCTGTTACTATTT    660
L  S  N  G  T  D  G  L  V  D  V  T  L  A  S  T  A  V  T  I
   170            175            180            185

CCAATAACCACTTCTTCGACCATGATGAAGTGATGTTGTTAGGACATAGTGATTCATTCT    720
S  N  N  H  F  F  D  H  D  E  V  M  L  L  G  H  S  D  S  F
   190            195            200            205

CAGATGATAAAGTGATGAAAGTCACAGTTGCATTTAACCACTTTGGACCTAATTGTGTGC    780
S  D  D  K  V  M  K  V  T  V  A  F  N  H  F  G  P  N  C  V
   210            215            220            225

AACGATTGCCAAGGGCTAGATATGGACACTTTCATGTTGTTAATAATAATTATGAGCCAT    840
Q  R  L  P  R  A  R  Y  G  H  F  H  V  V  N  N  N  Y  E  P
   230            235            240            245
```

Fig. 17 cont.

```
GGGGAAAATATGCCATTGGAGGAAGTTCTGATCCAACAATTATAAGTGAAGGGAATAGAT    900
W  G  K  Y  A  I  G  G  S  S  D  P  T  I  I  S  E  G  N  R
   250               255               260               265

TTCTTGCACCAAATGAATCTTATAAAAAGGAGGTGACAATACGTGTAGGTTGTAAATCTA    960
F  L  A  P  N  E  S  Y  K  K  E  V  T  I  R  V  G  C  K  S
   270               275               280               285

CAAGTTGTGATGCATGGGAGTGGAGATCAAAAGATGATGCCTTCCTTAATGGTGCCTATT   1020
T  S  C  D  A  W  E  W  R  S  K  D  D  A  F  L  N  G  A  Y
   290               295               300               305

TTGTACAATCAGGCAAGGGGTATAATGGTGGAGAGGCATTCAAGGTTGAAAGTGCAAATG   1080
F  V  Q  S  G  K  G  Y  N  G  G  E  A  F  K  V  E  S  A  N
   310               315               320               325

AGGTGCCAACATTGACTAAACATGCTGGAGCATTAAAATGTATACCTACCAAACAATGTG   1140
E  V  P  T  L  T  K  H  A  G  A  L  K  C  I  P  T  K  Q  C
   330               335               340               345

TGATATGAAAAGTCAATCGATATAATAATGTGTTATTTGTAATATTTCAGCTTTGAATAT   1200
V  I  -

GTATAGAAAAAGAATTTCAACAAAATGACACTATTATATAAATAAATTCTTAGTTTATTA   1260

GTTGGTATTAAAAAAAAA-3'                                          1278
```

Fig. 17 cont.

CJI-41	KMPMYIAGYKTFDGRGAQVYIGNGGPCVFI
CJI-41.1	PMYIAGYKTFDGRGAQVYIGNGGP
CJI-41.2	YIAGYKTFDGRGAQVYIGNGGP
CJI-41.3	KKYIAGYKTFDGRGAQVYIGNGGP

CJI-42	DALTLRTATNIWIDHNSFSNSSDGLVDVTL
CJI-42.1	RTATNIWIDHNSFSNSSDGLVD
CJI-42.2	KRTATNIWIDHNSFSNSSDGLVDK

CJI-43	KSMKVTVAFNQFGPNCGQRMPRARYGLVHVANNNYD
CJI-43.1	KSMKVTVAFNQFGPNCGQRMPRARYGLVHV
CJI-43.6	KSMKVTVAFNQFGPNSGQRMPRARYGLVHV
CJI-43.7	KSMKVTVAFNQFGPNCGQRMPRARYGLV
CJI-43.8	KSMKVTVAFNQFGPNSGQRMPRARYGLV
CJI-43.9	KSMKVTVAFNQFGPNCGQRMPRARYG
CJI-43.10	KSMKVTVAFNQFGPNSGQRMPRARYG
CJI-43.11	KSMKVTVAFNQFGPNSGQRMPRARYGKK
CJI-43.12	KSMKVTVAFNQFGPNCGQRMPRARYG

CJI-45	PRARYGLVHVANNNYDPWTIYAIGGSSNPT
CJI-45.1	RARYGLVHVANNNYDPWTIYAIGGSSNP
CJI-45.2	RARYGLVHVANNNYDPWTIYAIGGSS

CJI-44	DVFYNGAYFVSSGKYEGGNIYTKKEAFNVE
CJI-44.1	NGAYFVSSGKYEGGNIYTKKEAFNVE
CJI-44.2	NGAYFVSSGKYEGGNIYTKKEAFN
CJI-44.3	KKNGAYFVSSGKYEGGNIYTKKEAFN

Fig. 18

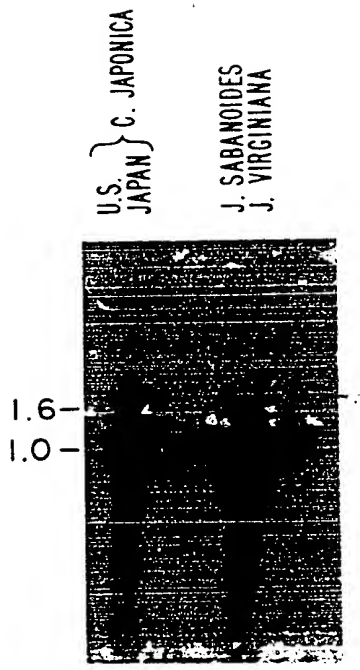


Fig. 19a

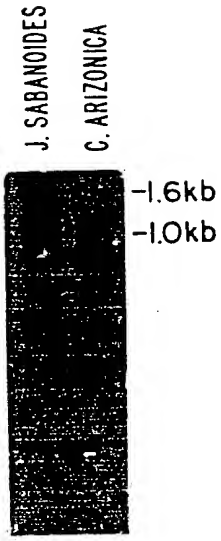


Fig. 19b

Fig. 20

CJI-42.5	DERTATNIWIDHNSFSNSSDD
CJI-42.8	DERTATNIWIDHNSFSNSSDGLAD
CJI-43.26	DEKSMKATVAFNQFGPNDE
CJI-43.27	DEKSMKVTAAFNQFGPNDE
CJI-43.30	DEEKSMKATVAFNEFGPNDEE
CJI-43.31	DEEKSMKVTVAANQFGPNDEE
CJI-43.32	DEEKSMKVTVAFNQAGPNDEE
CJI-43.35	DEKSMKATAAFNQFGPNDE
CJI-43.36	DEEKSMKATAAFNQFGPNDEE
CJI-43.39	DDAYSDDKSMKVTVAFNQFGDE
CJI-24.5	DKEPRARYGLVHVANNNYDPWTIEEE
CJI-44.5	DENGAYFVSSGKYEGGNIYTKKEAFNAE
CJI-44.6	DEENGAYFVSSGKYEGGNIYTKKEAFNVE
CJI-44.8	DEEGAYFVSSGKYEGGNIYTKKEAFNVE

Cry20.fig

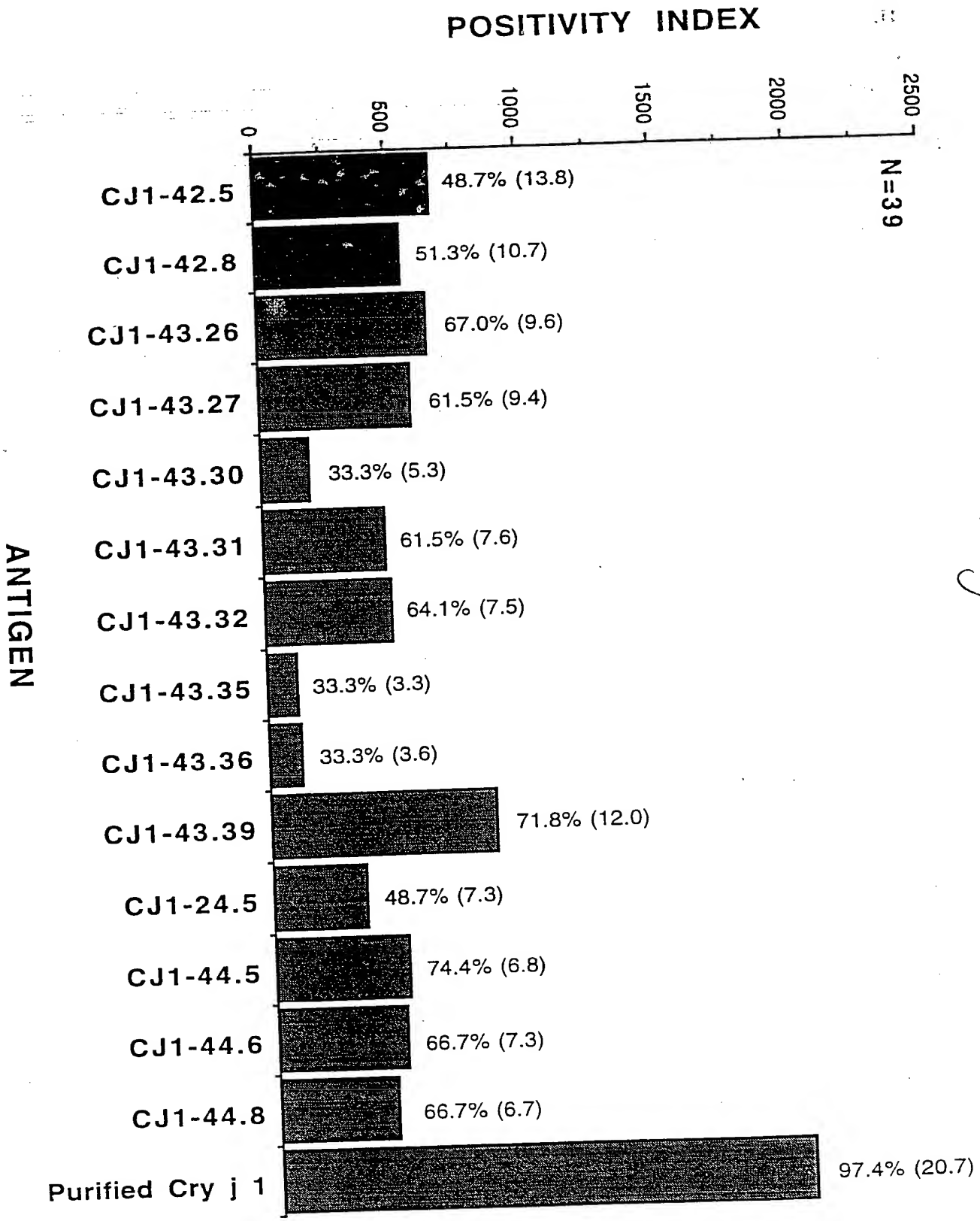

POSITIVITY INDEX
0
500
1000
1500
2000
2500
N=39
ANTIGEN
CJ1-42.5
48.7% (13.8)
CJ1-42.8
51.3% (10.7)
CJ1-43.26
67.0% (9.6)
CJ1-43.27
61.5% (9.4)
CJ1-43.30
33.3% (5.3)
CJ1-43.31
61.5% (7.6)
CJ1-43.32
64.1% (7.5)
CJ1-43.35
33.3% (3.3)
CJ1-43.36
33.3% (3.6)
CJ1-43.39
71.8% (12.0)
CJ1-24.5
48.7% (7.3)
CJ1-44.5
74.4% (6.8)
CJ1-44.6
66.7% (7.3)
CJ1-44.8
66.7% (6.7)
Purified Cry j 1
97.4% (20.7)

Fig. 21

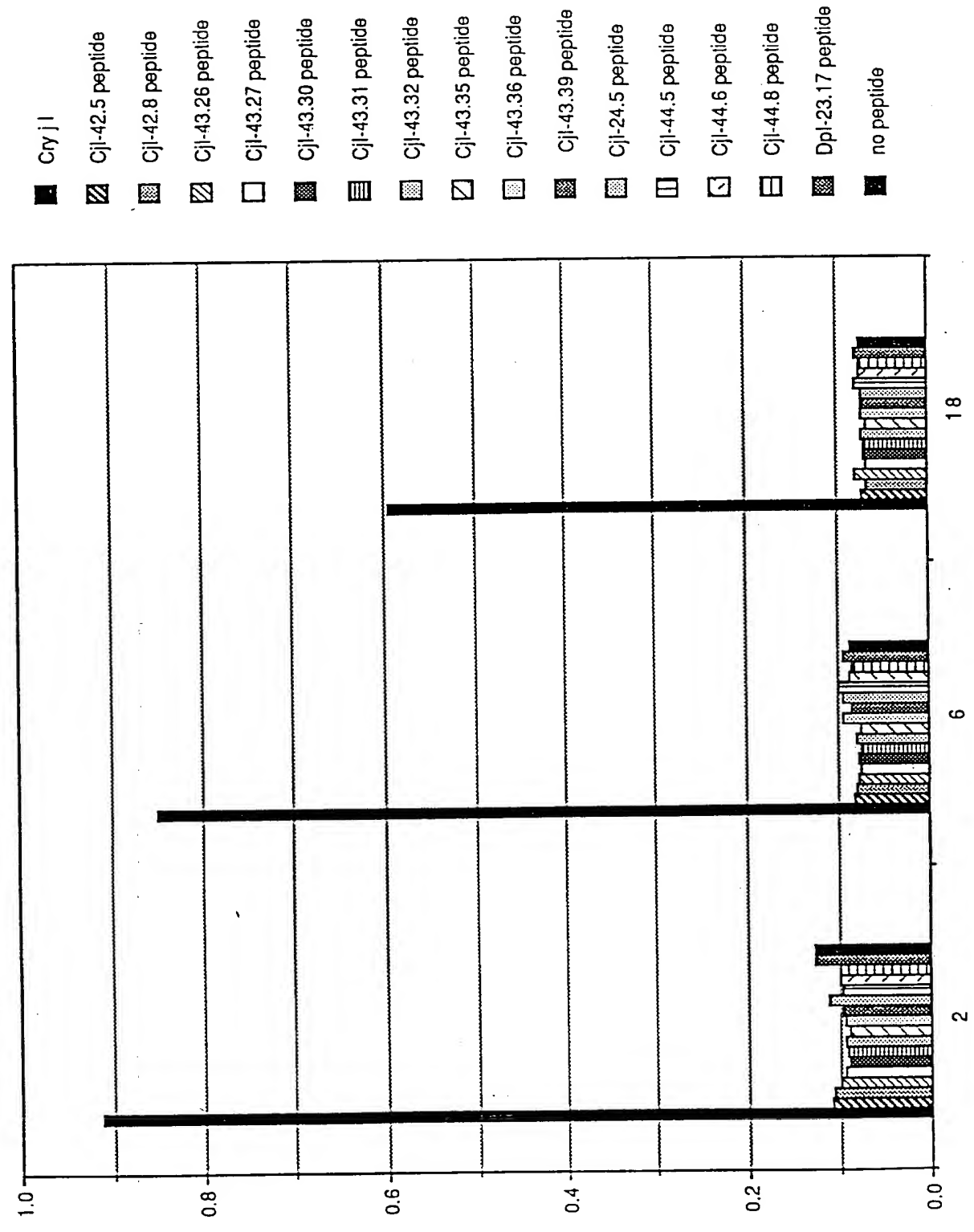

Cry j I
Cjl-42.5 peptide
Cjl-42.8 peptide
Cjl-43.26 peptide
Cjl-43.27 peptide
Cjl-43.30 peptide
Cjl-43.31 peptide
Cjl-43.32 peptide
Cjl-43.35 peptide
Cjl-43.36 peptide
Cjl-43.39 peptide
Cjl-24.5 peptide
Cjl-44.5 peptide
Cjl-44.6 peptide
Cjl-44.8 peptide
Dpl-23.17 peptide
no peptide
1.0
0.8
0.6
0.4
0.2
0.0
2
6
18
1/dilution of plasma

Fig. 22

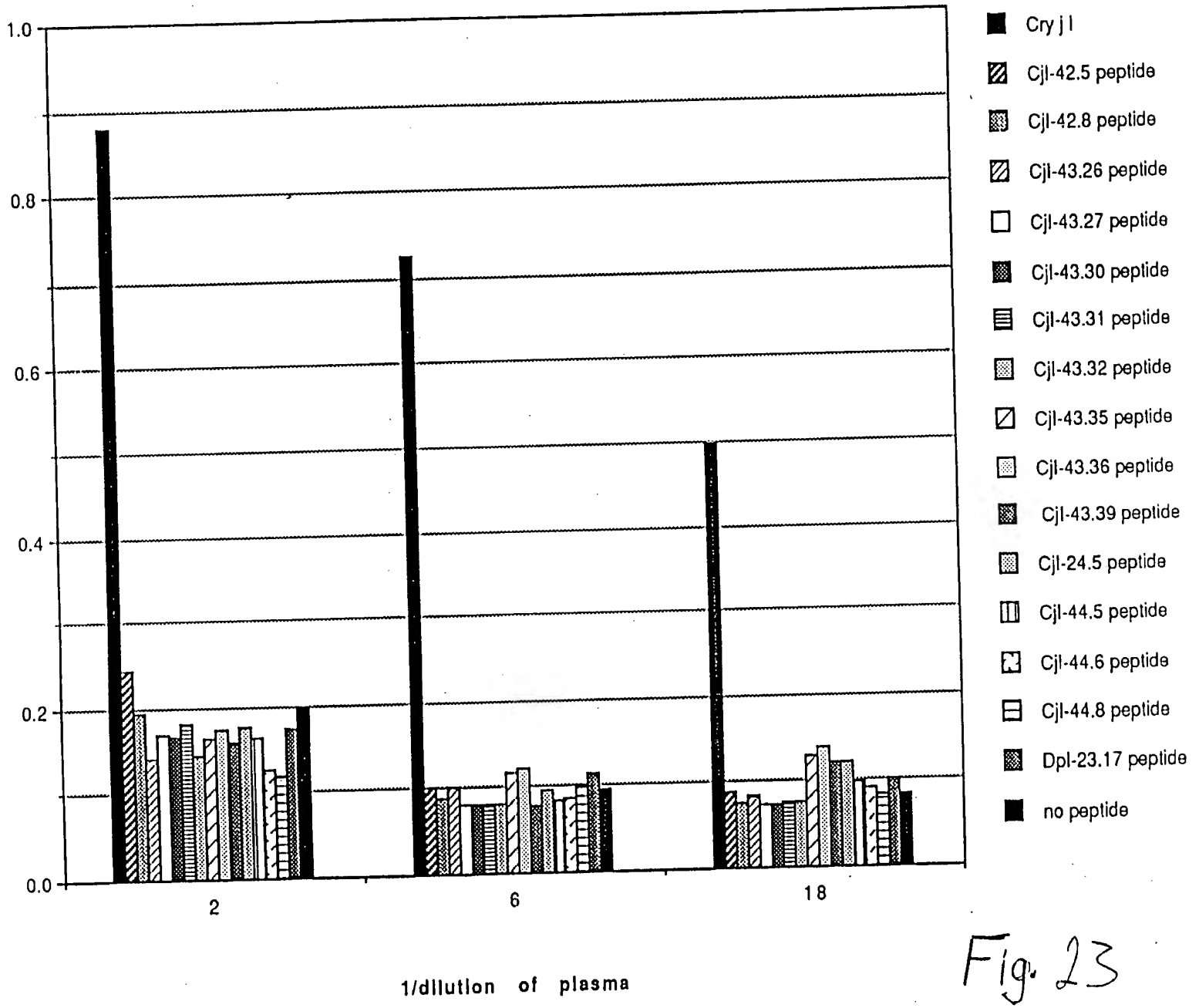


Fig. 23

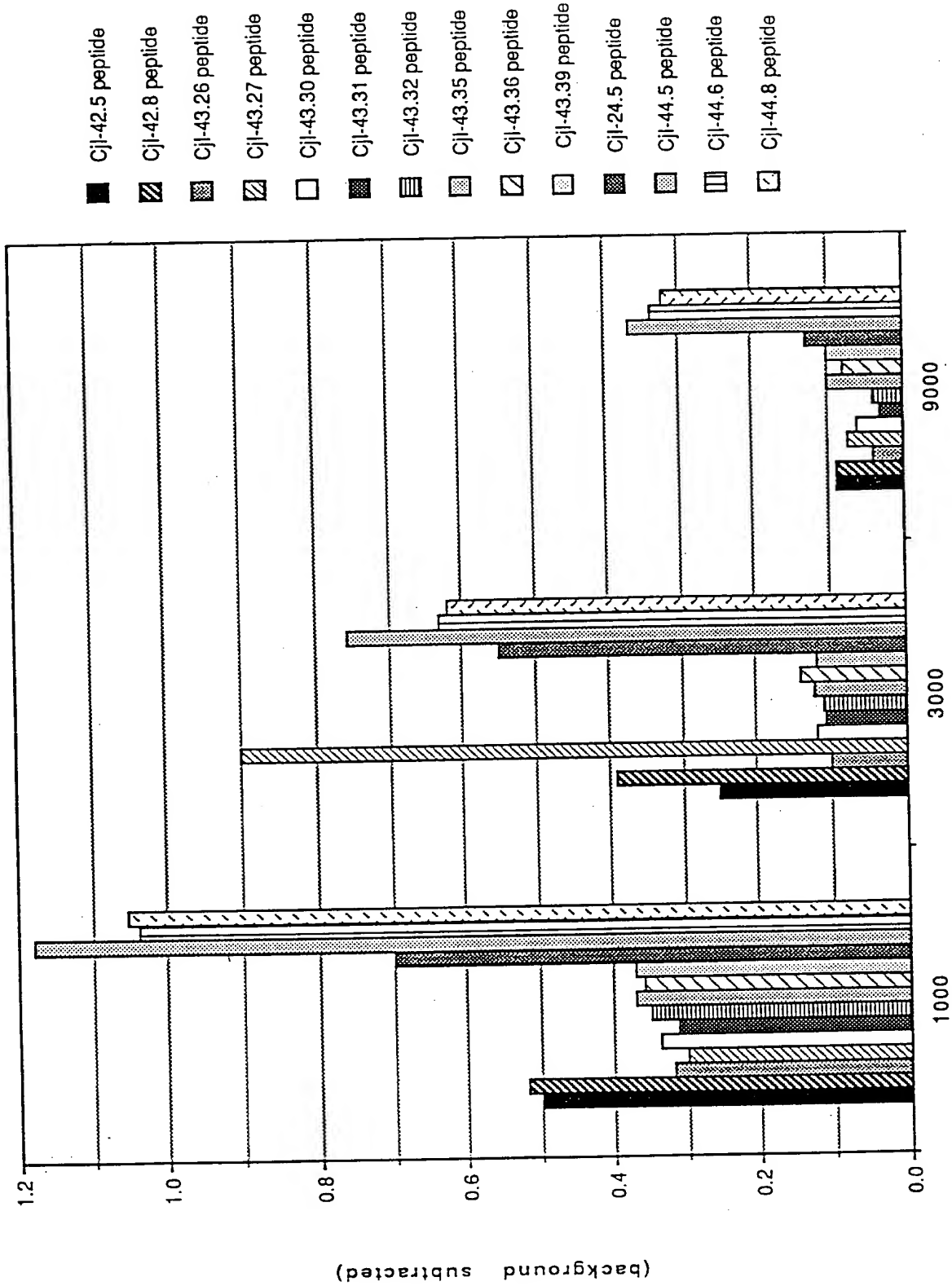

Cjl-42.5 peptide
Cjl-42.8 peptide
Cjl-43.26 peptide
Cjl-43.27 peptide
Cjl-43.30 peptide
Cjl-43.31 peptide
Cjl-43.32 peptide
Cjl-43.35 peptide
Cjl-43.36 peptide
Cjl-43.39 peptide
Cjl-24.5 peptide
Cjl-44.5 peptide
Cjl-44.6 peptide
Cjl-44.8 peptide
1.2
1.0
0.8
0.6
0.4
0.2
0.0
(background subtracted)
1000
3000
9000
1/dilution

Fig. 24

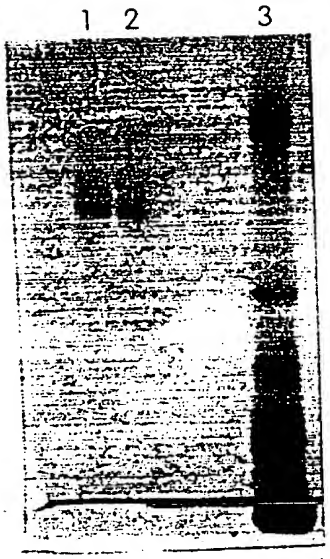


Fig. 25a

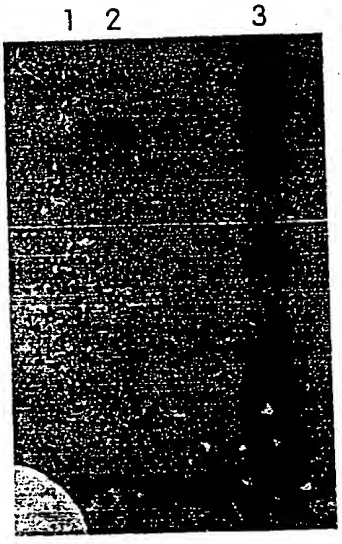


Fig. 25b

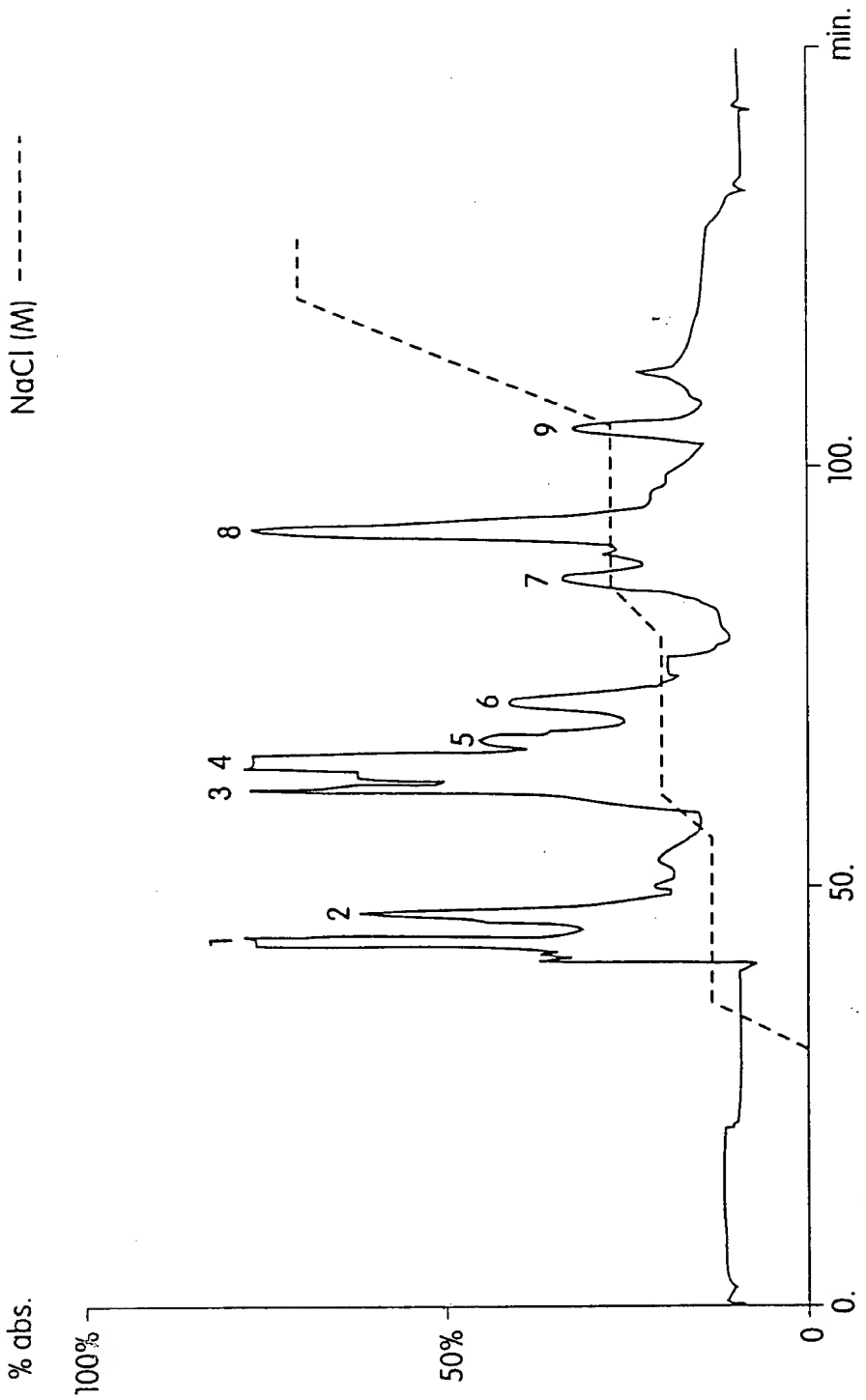


Fig. 26

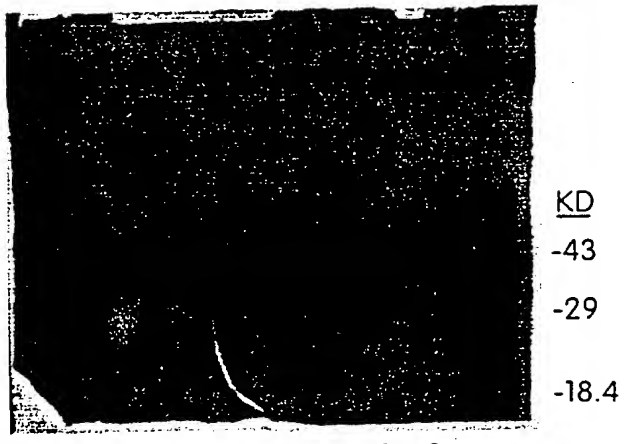


Fig. 27

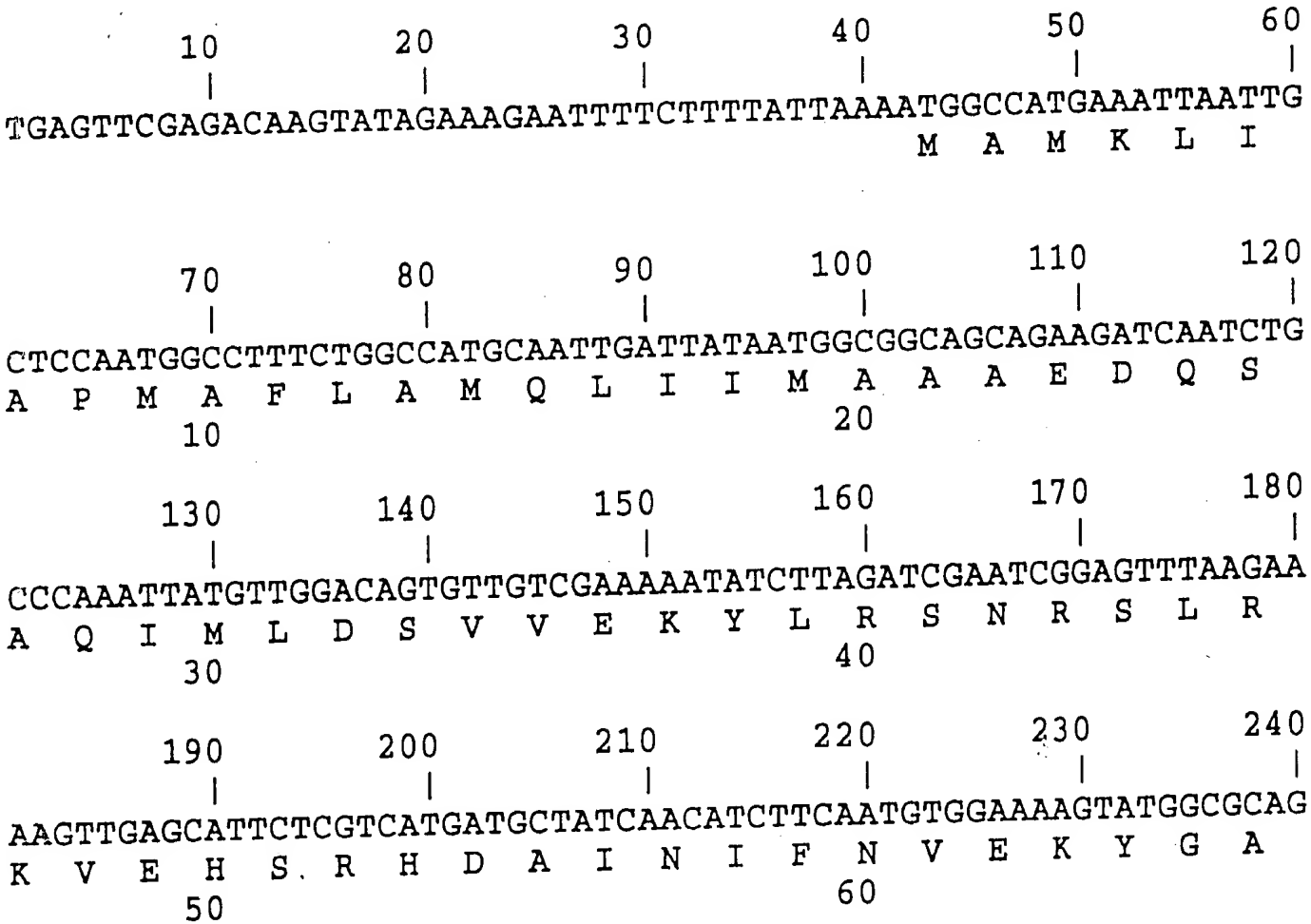


Fig. 28

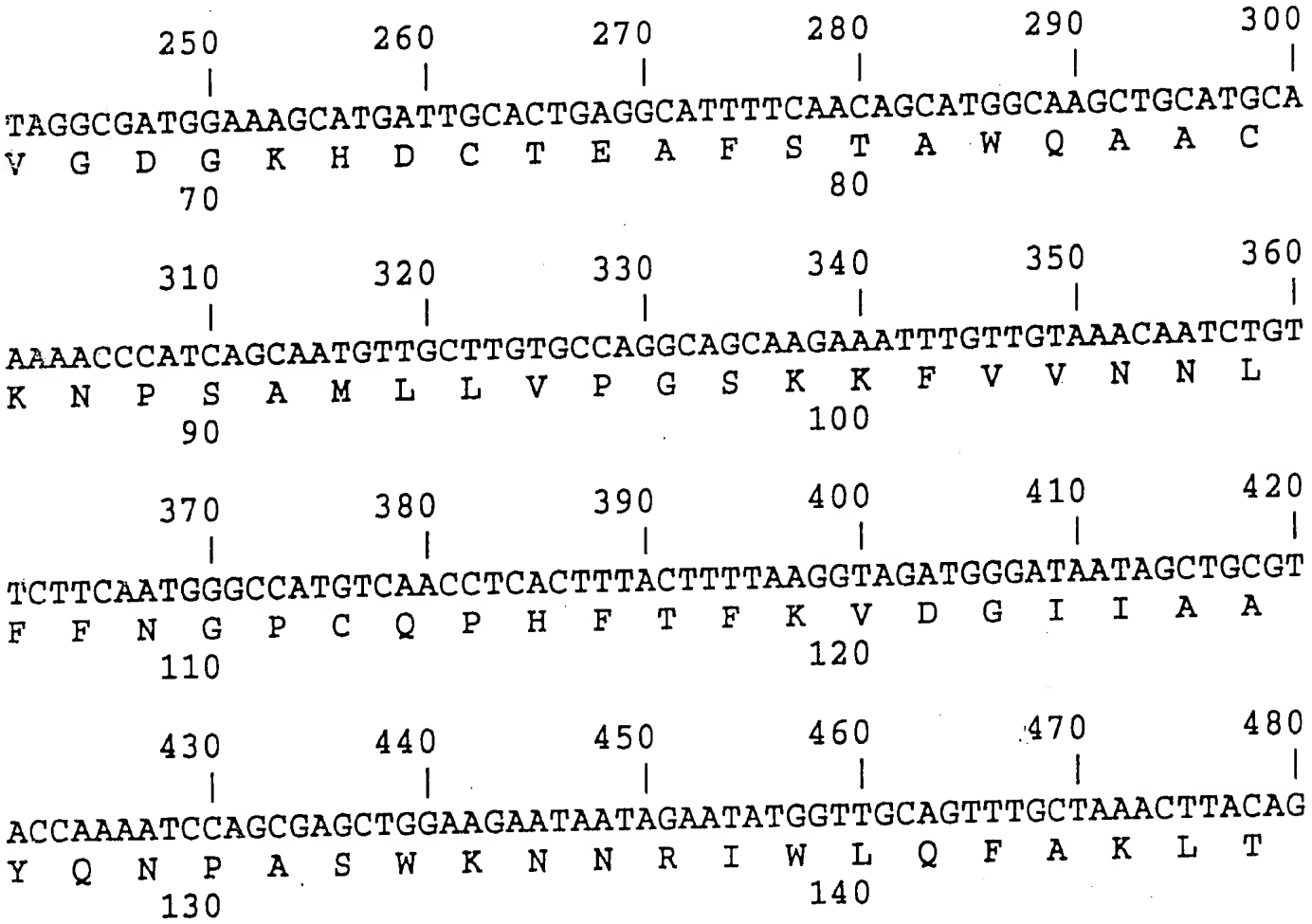


Fig. 28 Cont.

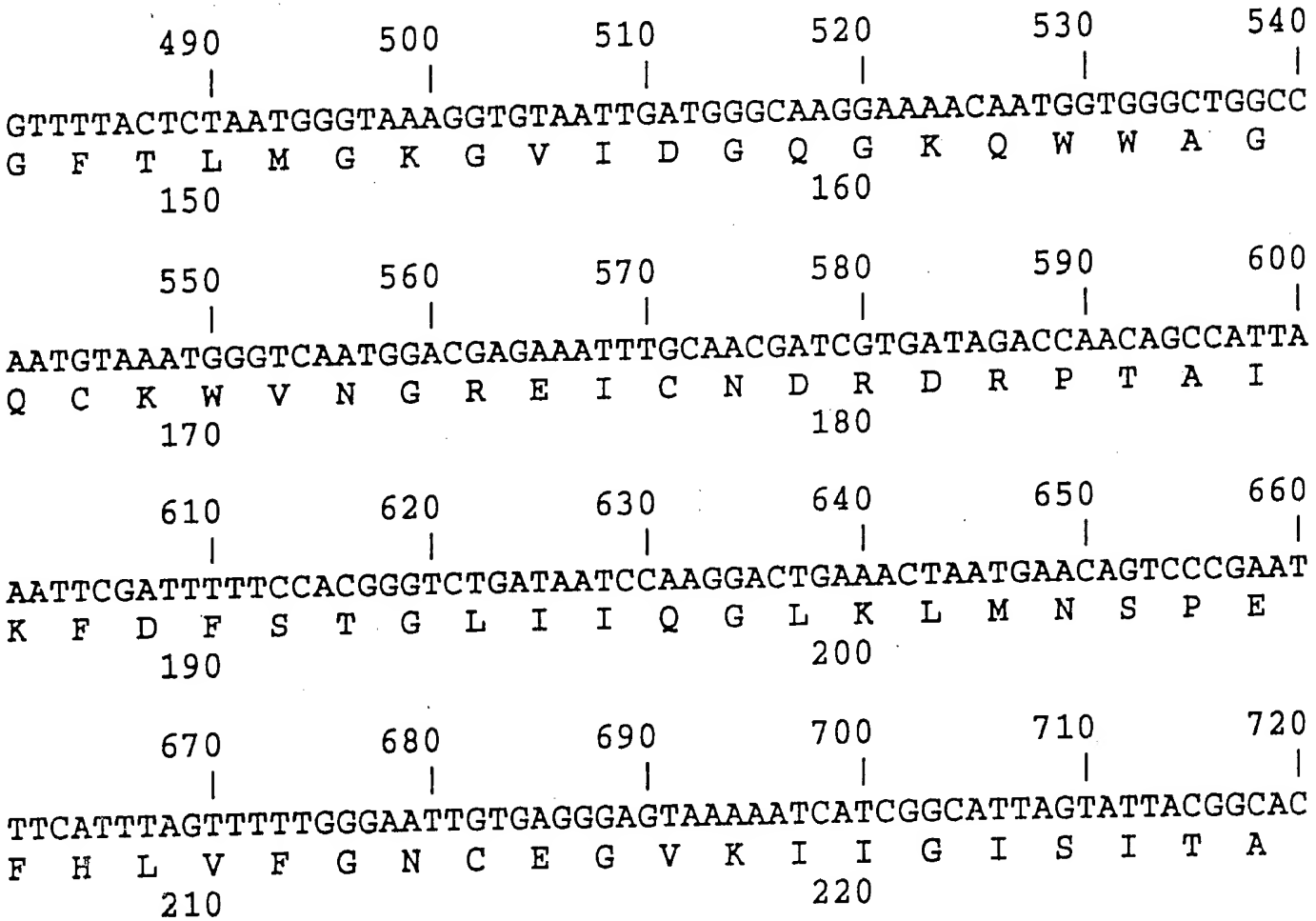


Fig.28 Cont.

```
        730         740         750         760         770         780
          |           |           |           |           |           |
CGAGAGACAGTCCTAACACTGATGGAATTGATATCTTTGCATCTAAAAACTTTCACTTAC
P  R  D  S  P  N  T  D  G  I  D  I  F  A  S  K  N  F  H  L
       230                                 240

        790         800         810         820         830         840
          |           |           |           |           |           |
AAAAGAACACGATAGGAACAGGGGATGACTGCGTCGCTATAGGCACAGGGTCTTCTAATA
Q  K  N  T  I  G  T  G  D  D  C  V  A  I  G  T  G  S  S  N
       250                                 260

        850         860         870         880         890         900
          |           |           |           |           |           |
TTGTGATTGAGGATCTGATTTGCGGTCCAGGCCATGGAATAAGTATAGGAAGTCTTGGGA
I  V  I  E  D  L  I  C  G  P  G  H  G  I  S  I  G  S  L  G
       270                                 280

        910         920         930         940         950         960
          |           |           |           |           |           |
GGGAAAACTCTAGAGCAGAGGTTTCATACGTGCACGTAAATGGGGCTAAATTCATAGACA
R  E  N  S  R  A  E  V  S  Y  V  H  V  N  G  A  K  F  I  D
       290                                 300
```

Fig.28 Cont.

```
        970         980         990        1000        1010        1020
          |           |           |           |           |           |
CACAAAATGGATTAAGAATCAAAACATGGCAGGGTGGTTCAGGCATGGCAAGCCATATAA
T  Q  N  G  L  R  I  K  T  W  Q  G  G  S  G  M  A  S  H  I
        310                                 320

        1030        1040        1050        1060        1070        1080
          |           |           |           |           |           |
TTTATGAGAATGTTGAAATGATAAATTCGGAGAACCCCATATTAATAAATCAATTCTACT
I  Y  E  N  V  E  M  I  N  S  E  N  P  I  L  I  N  Q  F  Y
        330                                 340

        1090        1100        1110        1120        1130        1140
          |           |           |           |           |           |
GCACTTCAGCTTCTGCTTGCCAAAACCAGAGGTCTGCGGTTCAAATCCAAGATGTGACAT
C  T  S  A  S  A  C  Q  N  Q  R  S  A  V  Q  I  Q  D  V  T
        350                                 360

        1150        1160        1170        1180        1190        1200
          |           |           |           |           |           |
ACAAGAACATACGTGGGACATCAGCAACAGCAGCAGCAATTCAACTTAAGTGCAGTGACA
Y  K  N  I  R  G  T  S  A  T  A  A  A  I  Q  L  K  C  S  D
        370                                 380
```

Fig. 28 Cont.

```
      1210        1220        1230        1240        1250        1260
        |           |           |           |           |           |
GTATGCCCTGCAAAGATATAAAGCTAAGTGATATATCTTTGAAGCTTACCTCAGGGAAAA
S  M  P  C  K  D  I  K  L  S  D  I  S  L  K  L  T  S  G  K
      390                                 400

      1270        1280        1290        1300        1310        1320
        |           |           |           |           |           |
TTGCTTCCTGCCTTAATGATAATGCAAATGGATATTTCAGTGGACACGTCATCCCTGCAT
I  A  S  C  L  N  D  N  A  N  G  Y  F  S  G  H  V  I  P  A
      410                                 420

      1330        1340        1350        1360        1370        1380
        |           |           |           |           |           |
GCAAGAATTTAAGTCCAAGTGCTAAGCGAAAAGAATCTAAATCCCATAAACACCCAAAAA
C  K  N  L  S  P  S  A  K  R  K  E  S  K  S  H  K  H  P  K
      430                                 440

      1390        1400        1410        1420        1430        1440
        |           |           |           |           |           |
CTGTAATGGTTGAAAATATGCGAGCATATGACAAGGGTAACAGAACACGCATATTGTTGG
T  V  M  V  E  N  M  R  A  Y  D  K  G  N  R  T  R  I  L  L
      450                                 460
```

Fig.28 Cont.

```
      1450       1460       1470       1480       1490       1500
        |          |          |          |          |          |
GGTCGAGGCCTCCGAATTGTACAAACAAATGTCATGGTTGCAGTCCATGTAAGGCCAAGT
G  S  R  P  P  N  C  T  N  K  C  H  G  C  S  P  C  K  A  K
      470                                 480

      1510       1520       1530       1540       1550       1560
        |          |          |          |          |          |
TAGTTATTGTTCATCGTATTATGCCGCAGGAGTATTATCCTCAGAGGTGGATATGCAGCT
L  V  I  V  H  R  I  M  P  Q  E  Y  Y  P  Q  R  W  I  C  S
      490                                 500

      1570       1580       1590       1600       1610       1620
        |          |          |          |          |          |
GTCATGGCAAAATCTACCATCCATAATGAGATACATTGAAACTGTATGTGCTAGTGAATA
C  H  G  K  I  Y  H  P  -
      510        514

      1630       1640       1650       1660       1670       1680
        |          |          |          |          |          |
TTCTTGTGGTACAATATTAGAACTGATATTGAAAATAAATCATCAATGTTTCTAAGGCAT


      1690       1700       1710       1720
        |          |          |          |
TTATAATAGATTATATTAATGGTTCAGCCTGGTGCAAAAAAAAAAA
```

Fig.28 Cont.

```
         10         20         30         40         50
          |          |          |          |          |
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSLRKVEH

         60         70         80         90        100
          |          |          |          |          |
SRHDAINIFNVEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKK

        110        120        130        140        150
          |          |          |          |          |
FVVNNLFFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWLQFAKLTGFTL

        160        170        180        190        200
          |          |          |          |          |
MGKGVIDGQGKQWWAGQCKWVNGREICNDRDRPTAIKFDFSTGLIIQGLK

        210        220        230        240        250
          |          |          |          |          |
LMNSPEFHLVFGNCEGVKIIGISITAPRDSPNTDGIDIFASKNFHLQKNT

        260        270        280        290        300
          |          |          |          |          |
IGTGDDCVAIGTGSSNIVIEDLICGPGHGISIGSLGRENSRAEVSYVHVN

        310        320        330        340        350
          |          |          |          |          |
GAKFIDTQNGLRIKTWQGGSGMASHIIYENVEMINSENPILINQFYCTSA

        360        370        380        390        400
          |          |          |          |          |
SACQNQRSAVQIQDVTYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISL

        410        420        430        440        450
          |          |          |          |          |
KLTSGKIASCLNDNANGYFSGHVIPACKNLSPSAKRKESKSHKHPKTVMV

        460        470        480        490        500
          |          |          |          |          |
ENMRAYDKGNRTRILLGSRPPNCTNKCHGCSPCKAKLVIVHRIMPQEYYP

        510  514
          |    |
QRWICSCHGKIYHP
```

Fig. 29

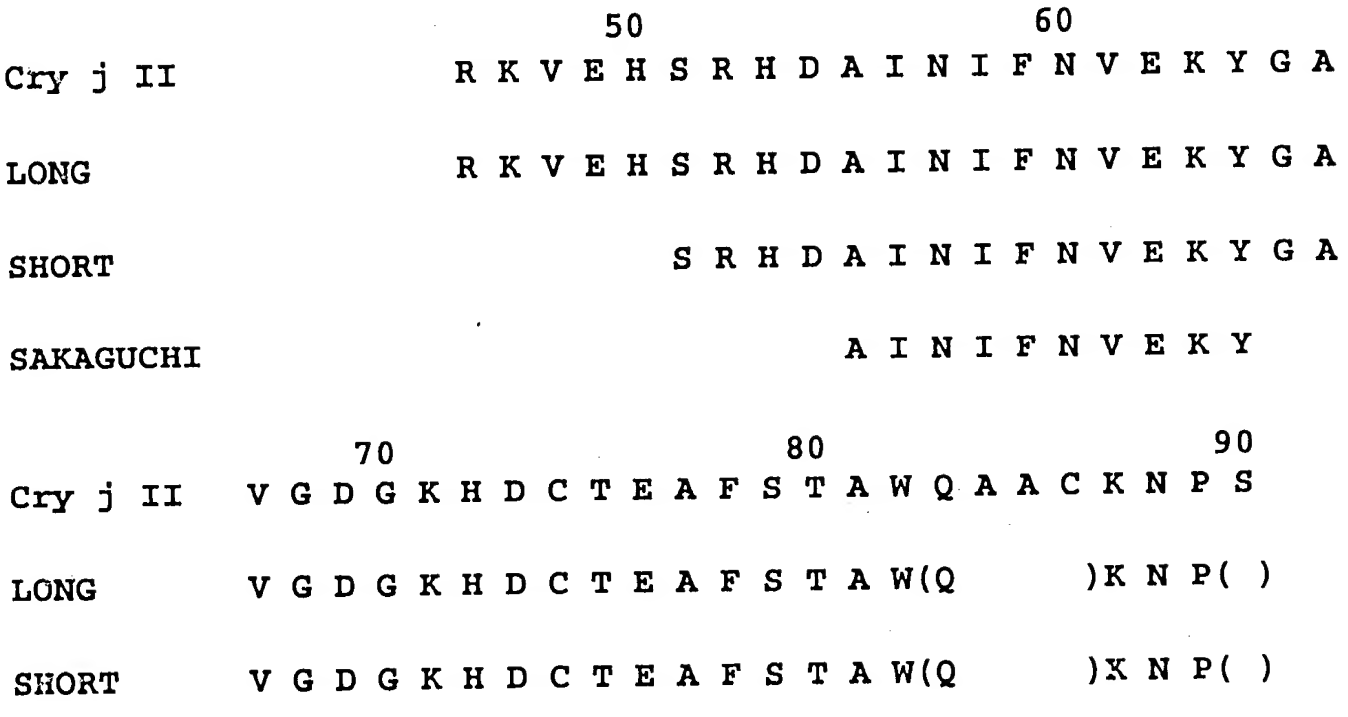


Fig 30

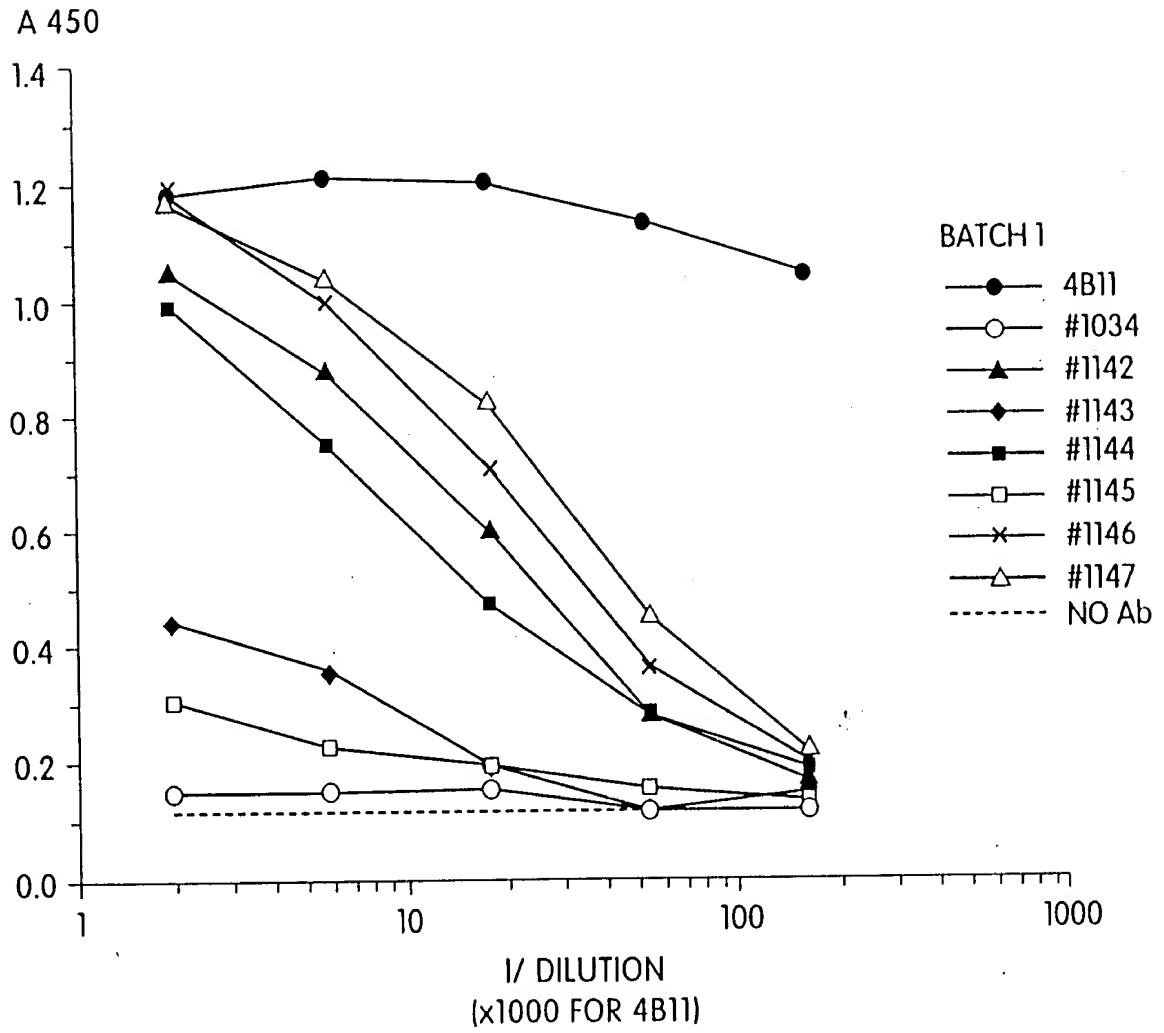


Fig. 31

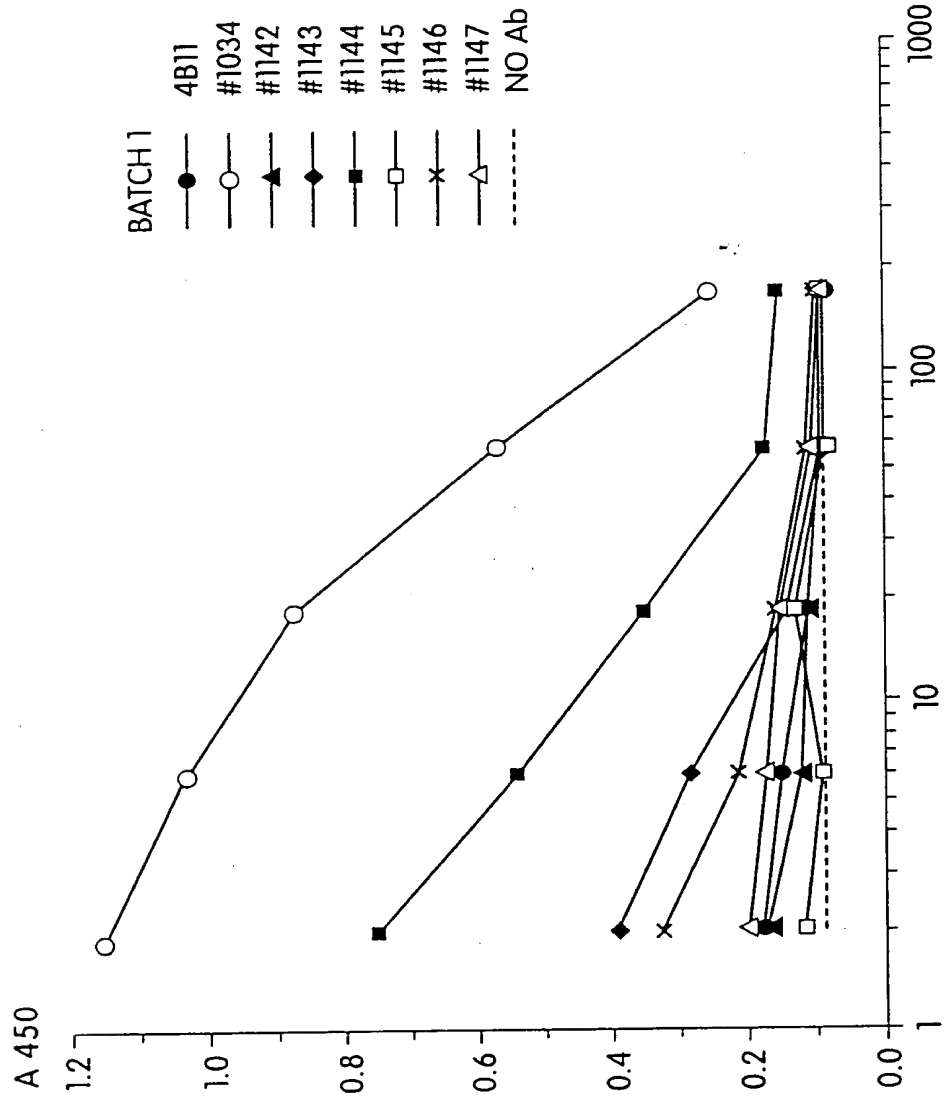

A 450
1.2
1.0
0.8
0.6
0.4
0.2
0.0
1
10
100
1000
1/ DILUTION
(x1000 FOR 4B11)
BATCH 1
4B11
#1034
#1142
#1143
#1144
#1145
#1146
#1147
NO Ab

Fig. 32

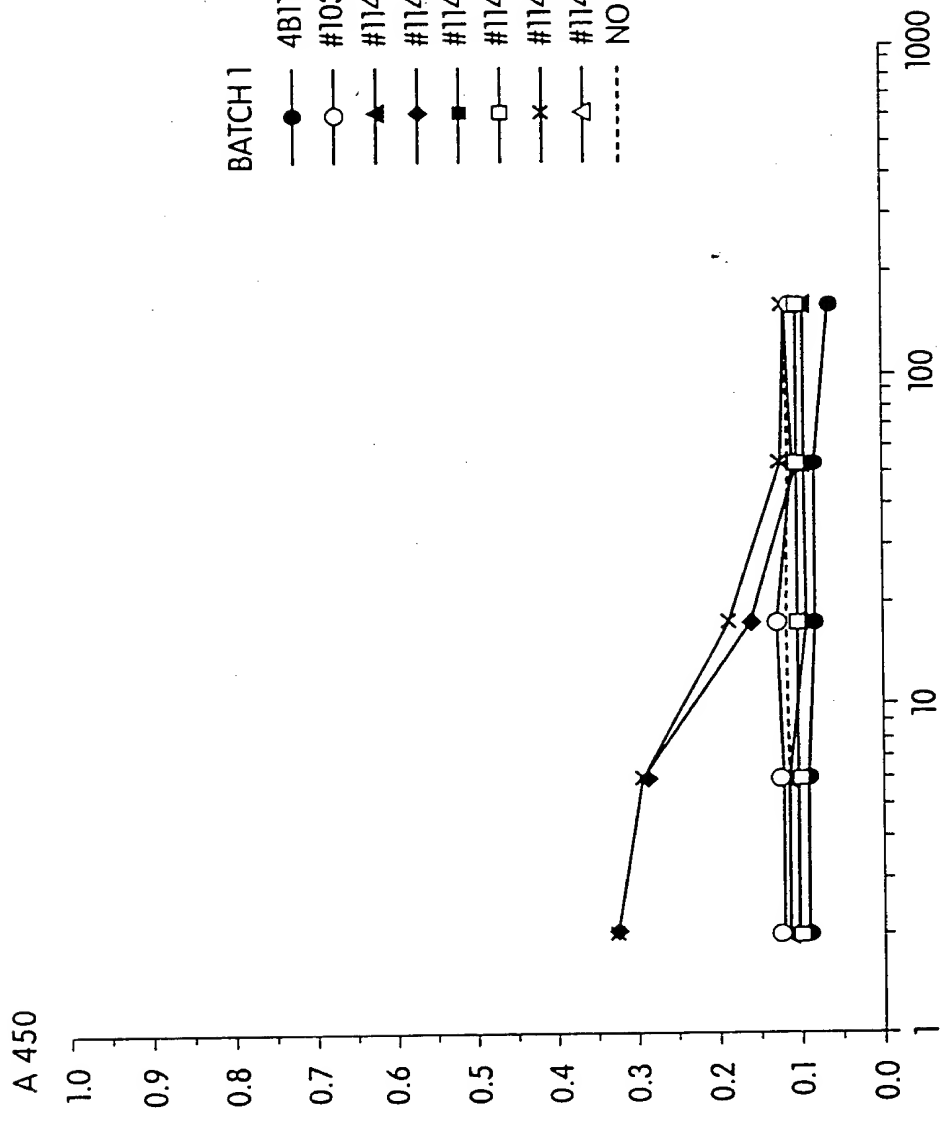

A 450
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
1
10
100
1000
1/ DILUTION
(x1000 FOR 4B11)
BATCH 1
4B11
#1034
#1142
#1143
#1144
#1145
#1146
#1147
NO Ab

Fig. 33

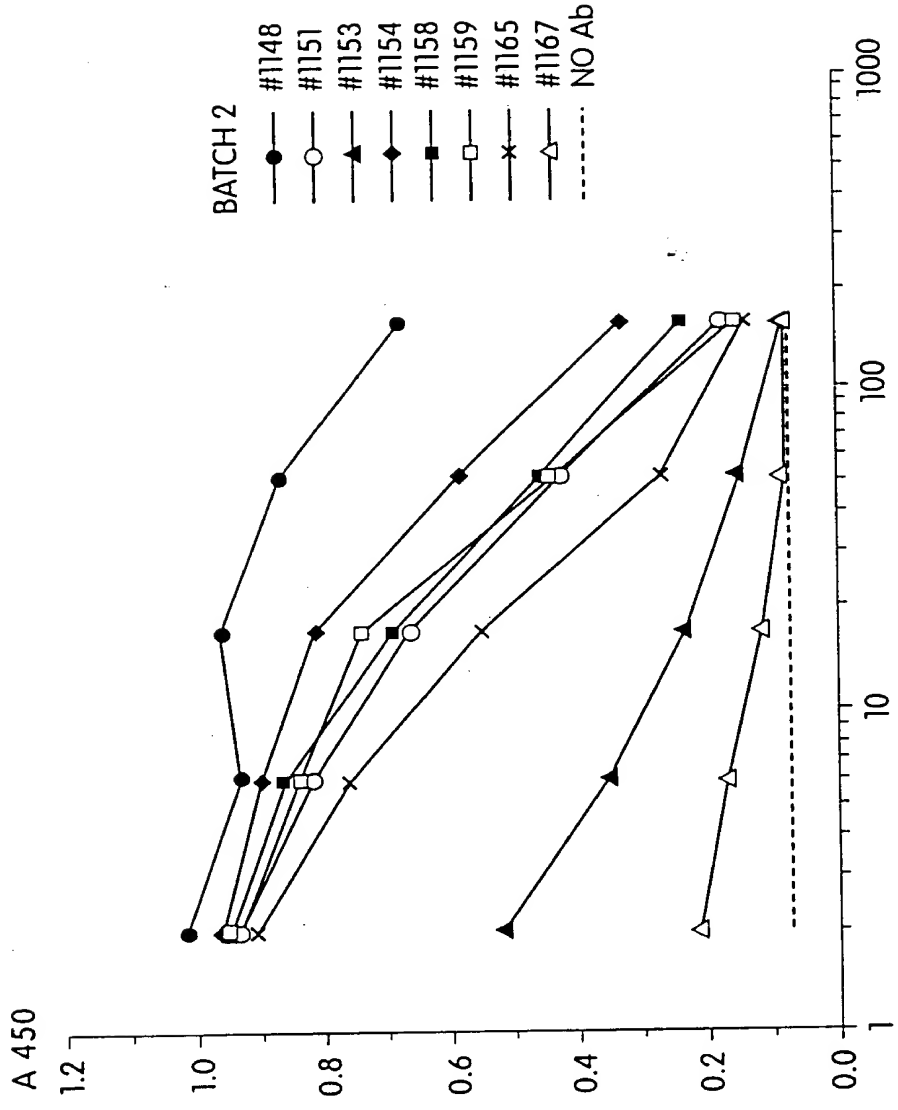

A 450
1.2
1.0
0.8
0.6
0.4
0.2
0.0
1
10
100
1000
1/ DILUTION
BATCH 2
#1148
#1151
#1153
#1154
#1158
#1159
#1165
#1167
NO Ab

Fig. 34

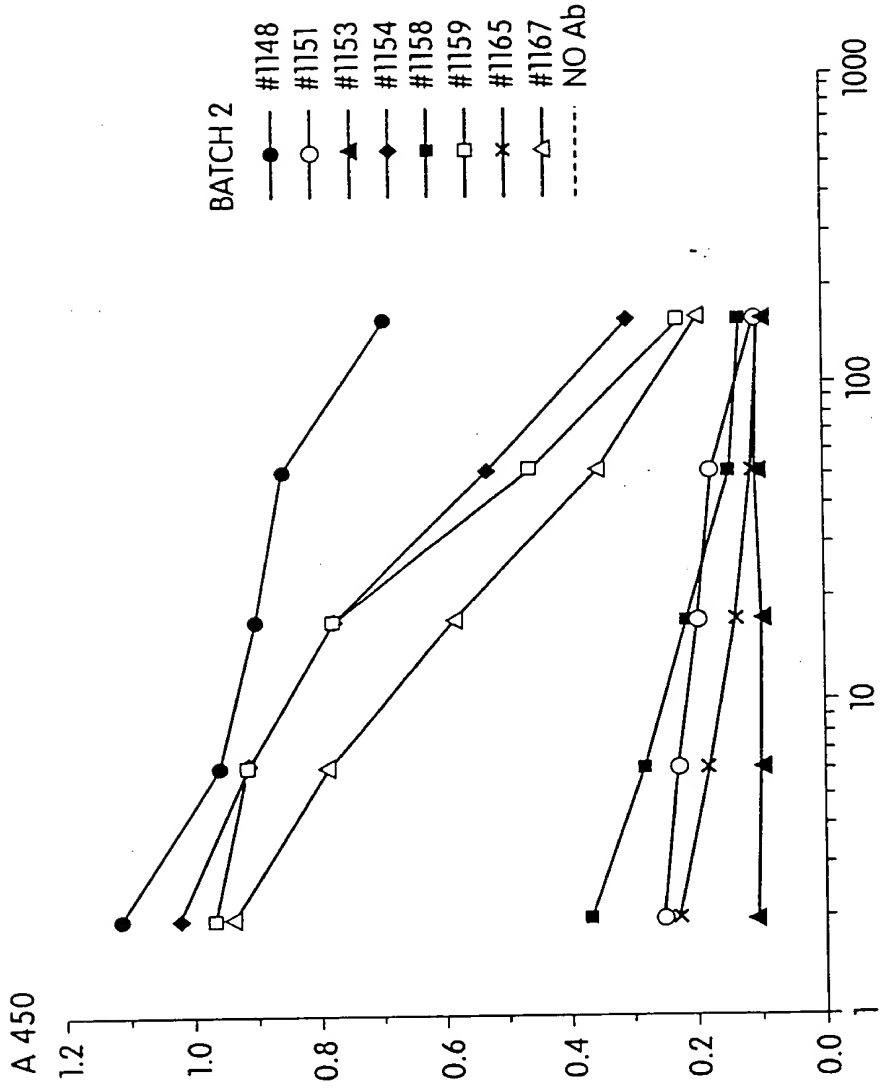

A 450
1.2
1.0
0.8
0.6
0.4
0.2
0.0
1
10
100
1000
1/ DILUTION
BATCH 2
#1148
#1151
#1153
#1154
#1158
#1159
#1165
#1167
NO Ab

Fig. 35

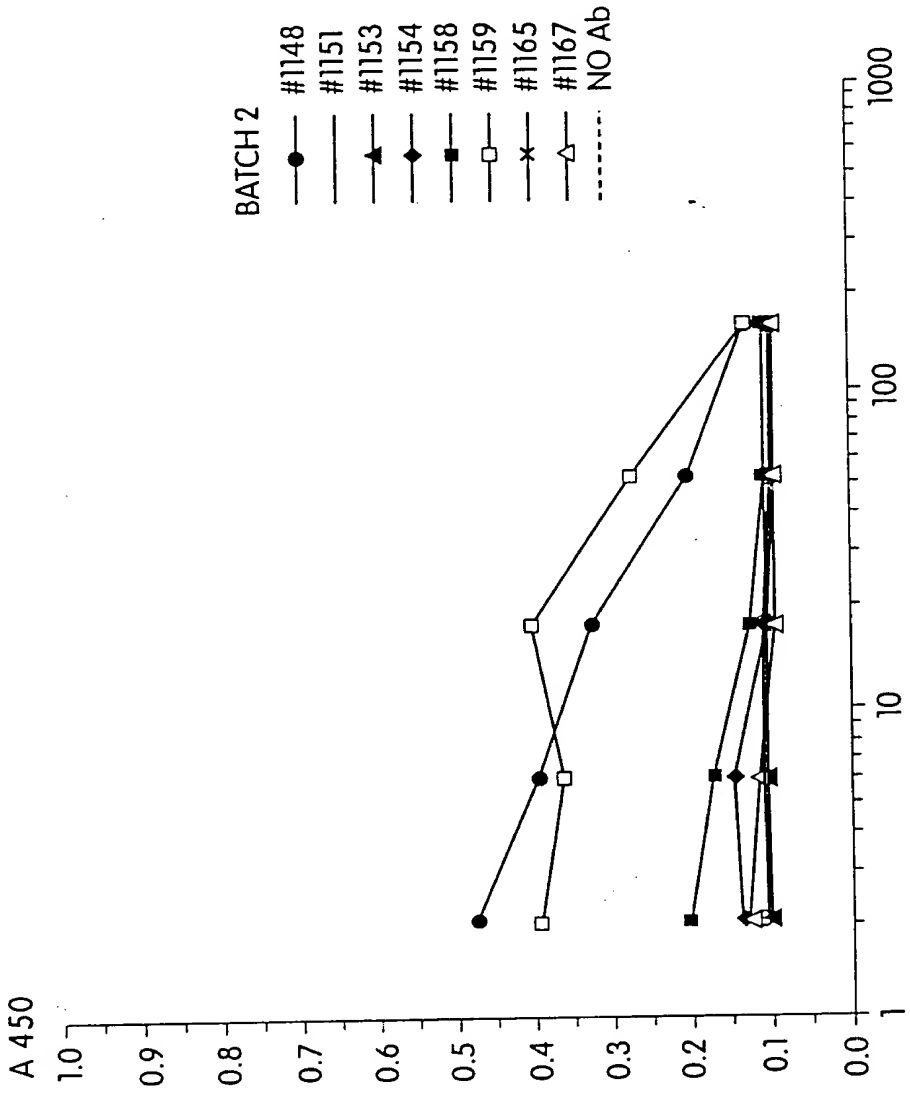

A 450
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
1
10
100
1000
1/ DILUTION
BATCH 2
#1148
#1151
#1153
#1154
#1158
#1159
#1165
#1167
NO Ab

Fig. 36

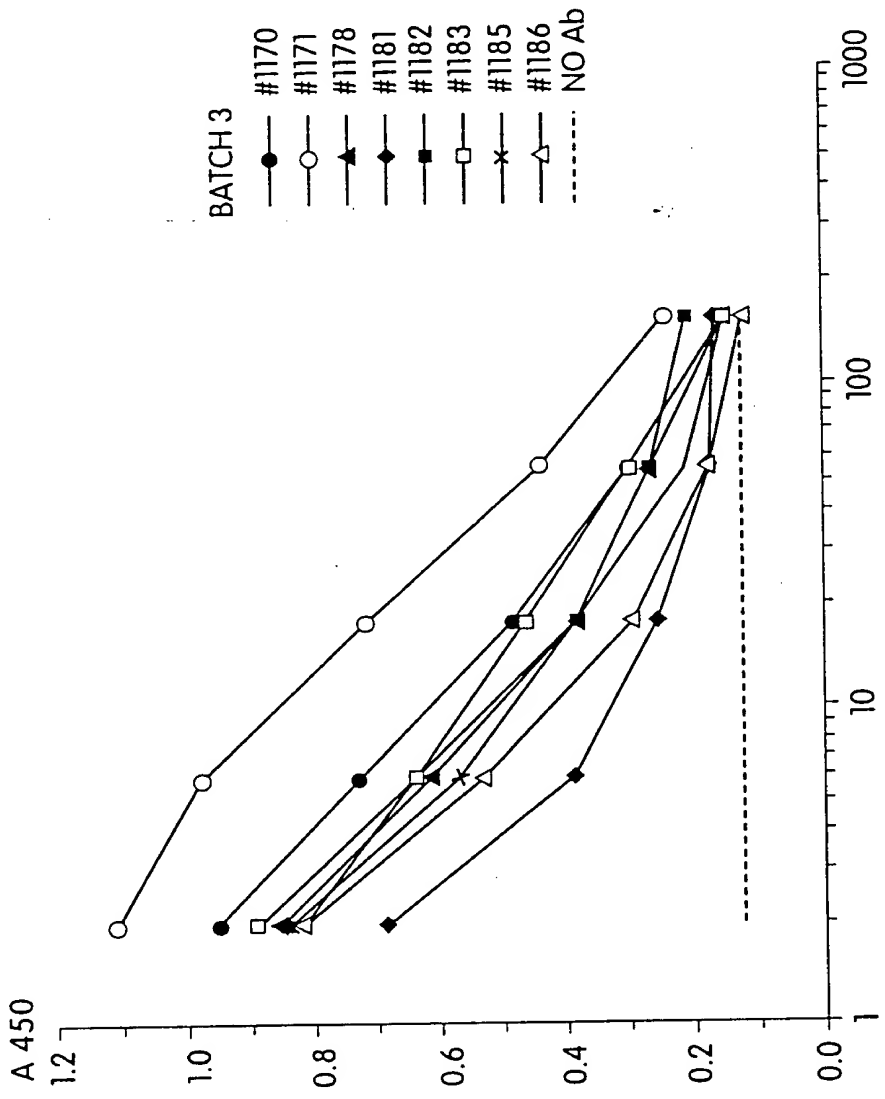

BATCH 3
#1170
#1171
#1178
#1181
#1182
#1183
#1185
#1186
NO Ab
A 450
1.2
1.0
0.8
0.6
0.4
0.2
0.0
1
10
100
1000
1/ DILUTION

Fig. 37

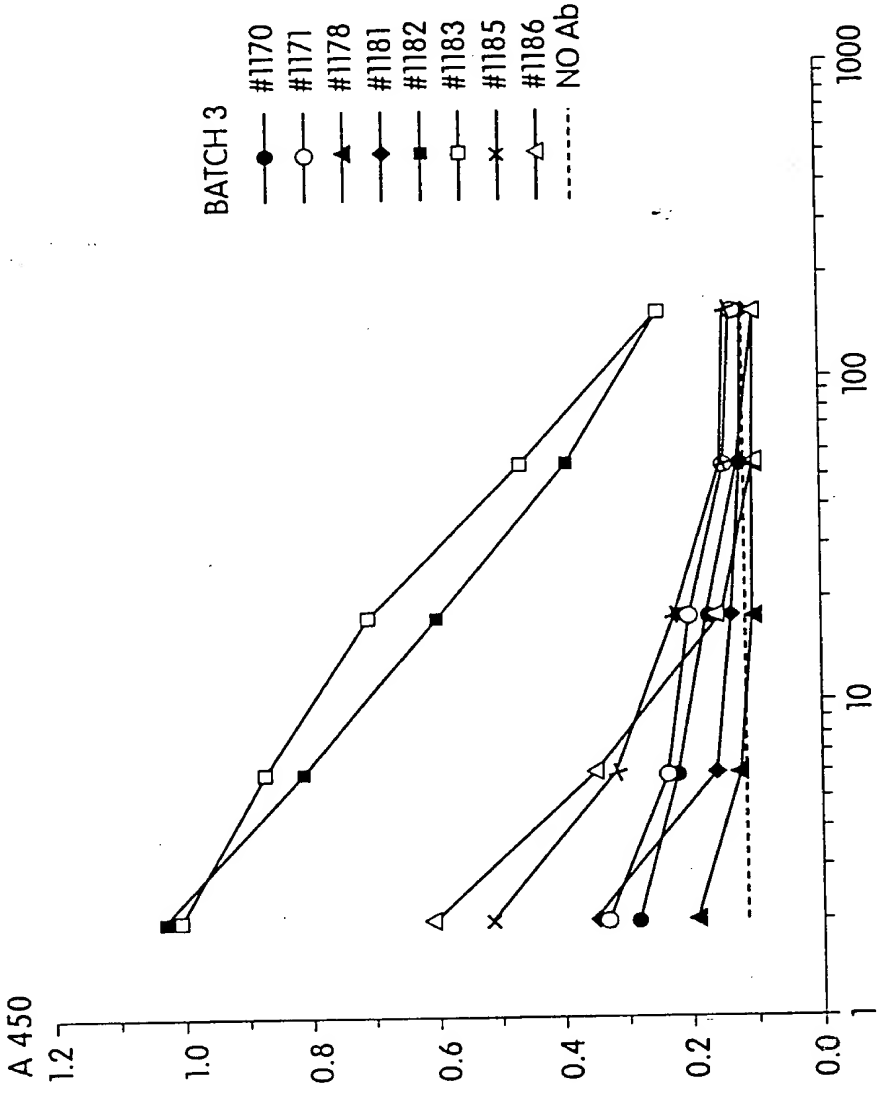

BATCH 3
#1170
#1171
#1178
#1181
#1182
#1183
#1185
#1186
NO Ab
A 450
1.2
1.0
0.8
0.6
0.4
0.2
0.0
1
10
100
1000
1/ DILUTION

Fig. 38

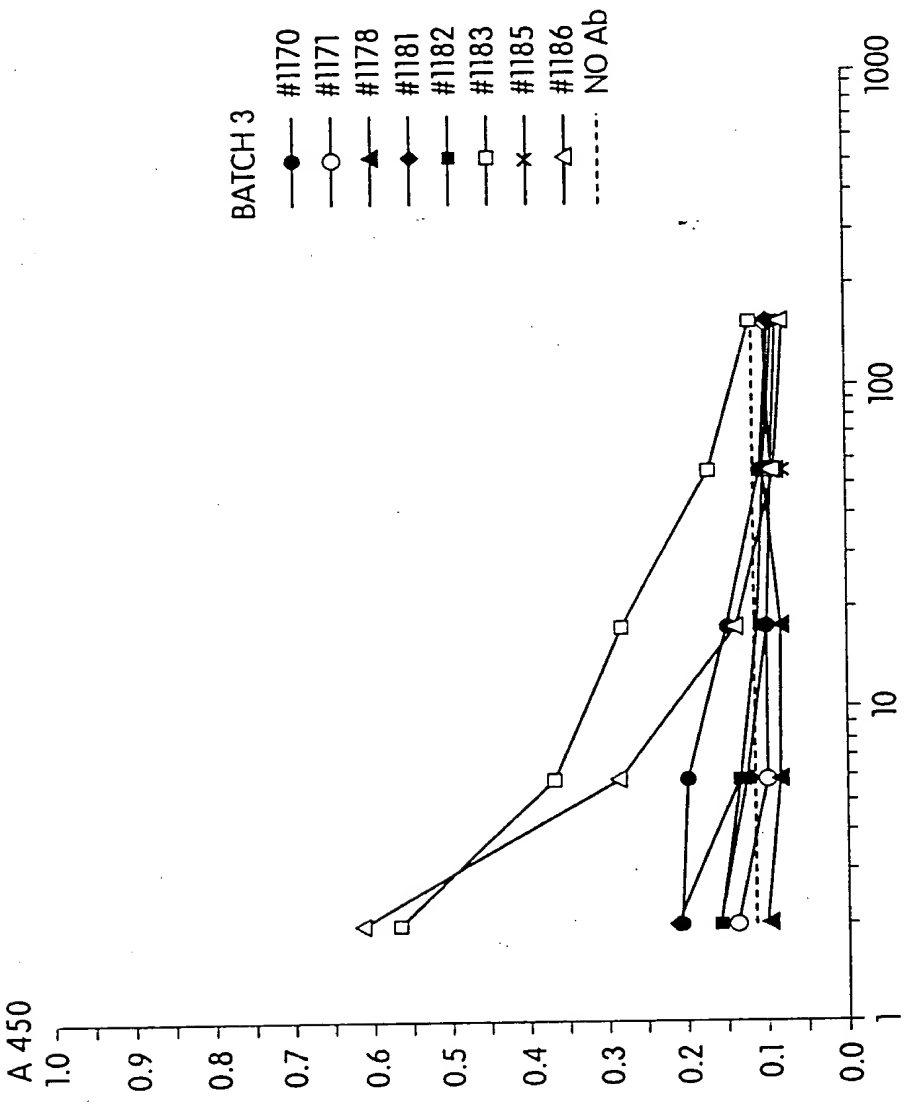

A 450
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
1
10
100
1000
1/ DILUTION
BATCH 3
#1170
#1171
#1178
#1181
#1182
#1183
#1185
#1186
NO Ab

Fig. 39

PATIENT #	MAST	PURIFIED NATIVE Cry j I	PURIFIED NATIVE Cry j II	RECOMBINANT Cry j II (rCry j II)
1034	2	-	+	-
1142	2	+	-	-
1143	0	+	+	+
1144	1	+	+	-
1145	0	-	-	+
1146	3	+	-	-
1147	3	+	-	-
1148	3	+	+	+
1151	3	+	+	-
1153	1	+	-	-
1154	3	+	+	-
1158	2	+	+	-
1159	2	+	+	+
1165	1	+	-	+
1167	1/0	-	+	-
1170	1/0	+	-	-
1171	2	+	-	-
1178	1	+	-	-
1181	1/0	+	-	-
1182	1	+	+	-
1183	1	+	+	+
1185	1/0	+	+	-
1186	1/0	+	+	+
POSITIVE	21	20	13	5

Fig. 40

FIG. 41

Cry j IIA FTFKVDGIIAAYQ

Cry j IIB NGYFSGHVIPACKN

Cry j IIC:

```
1         10         20         30         40         50         60
|         |          |          |          |          |          |
MGHHHHHHEFRKVEHSRHDAINIFNVEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLV

          70         80         90         100        110        120
          |          |          |          |          |          |
PGSKKFVVNNLFFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWLQFAKLTGFTLMGKGV

      128
       |
IDGQGKQW
```

Cry j IID:

```
1         10         20         30         40         50         60
|         |          |          |          |          |          |
MGHHHHHHEFWAGQCKWVNGREICNDRDRPTAIKFDFSTGLIIQGLKLMNSPEFHLVFGN

          70         80         90         100        110        120
          |          |          |          |          |          |
CEGVKIIGISITAPRDSPNTDGIDIFASKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLI

     127
      |
CGPGHGI
```

Fig. 41 Cont.

Cry j IIE:

```
1         10         20         30         40         50         60
|         |          |          |          |          |          |
MGHHHHHHEFSIGSLGRENSRAEVSYVHVNGAKFIDTQNGLRIKTWQGGSGMASHIIYEN

          70         80         90        100        110        120
          |          |          |          |          |          |
VEMINSENPILINQFYCTSASACQNQRSAVQIQDVTYKNIRGTSATAAAIQLKCSDSMPC

     127
      |
KDIKLSD
```

Cry j IIF:

```
1         10         20         30         40         50         60
|         |          |          |          |          |          |
MGHHHHHHEFISLKLTSGKIASCLNDNANGYFSGHVIPACKNLSPSAKRKESKSHKHPKT

          70         80         90        100        110        120
          |          |          |          |          |          |
VMVENMRAYDKGNRTRILLGSRPPNCTNKCHGCSPCKAKLVIVHRIMPQEYYPQRWICSC

     127
      |
HGKIYHP
```

Cry j IIG (J1) GKGVIDGQGKQWWAGQCKWVNGRE

Cry j-IIH (J3) DSMPCKDIKLSDISLKLTSGKIAS

Cry j-IIQ (J2) IEDLICGPGHGISIGSLGRENSRA

Cry41.Fig

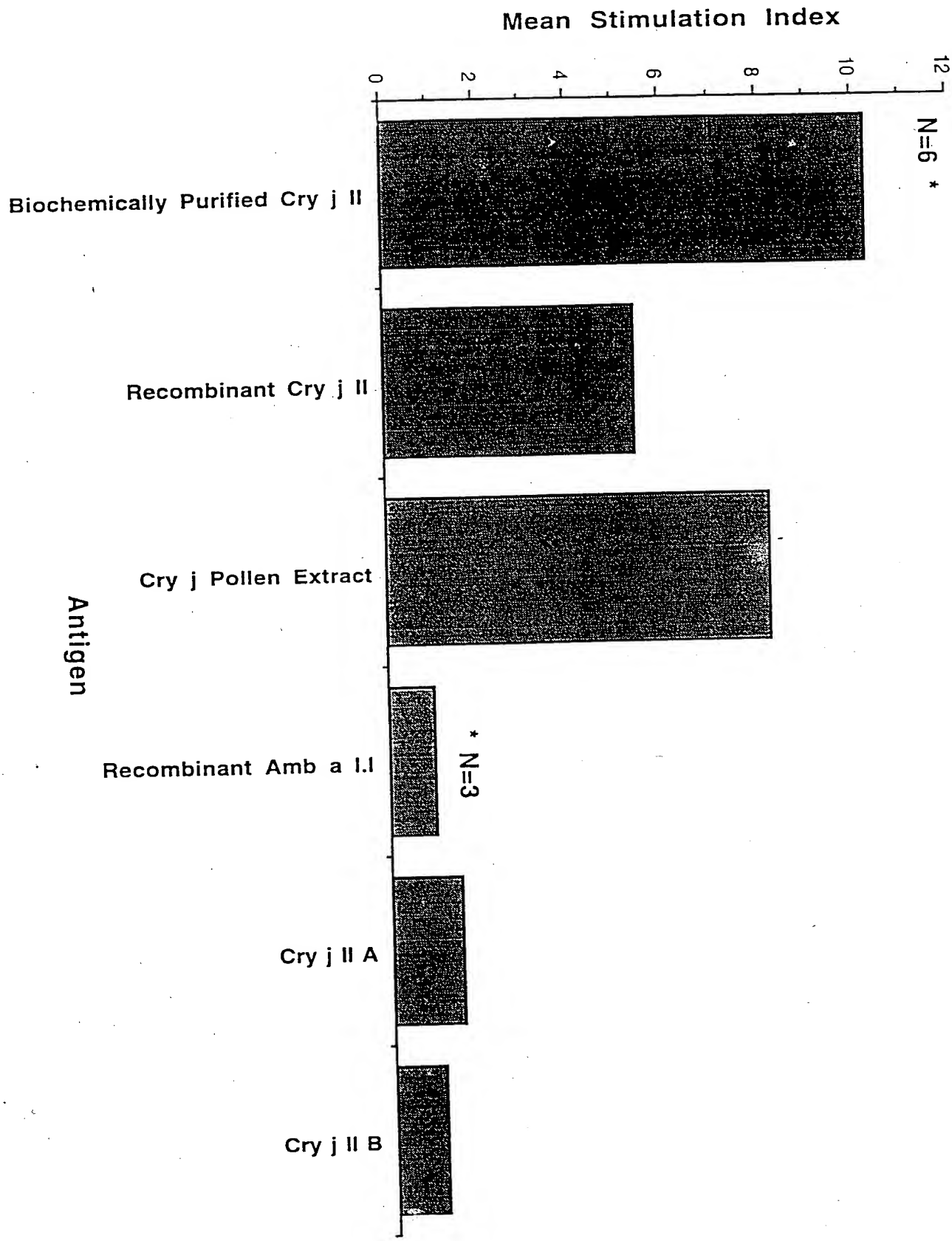

Mean Stimulation Index
0
2
4
6
8
10
12
Biochemically Purified Cry j II
N=6 *
Recombinant Cry j II
Cry j Pollen Extract
Recombinant Amb a I.I
* N=3
Cry j II A
Cry j II B
Antigen

Fig 42

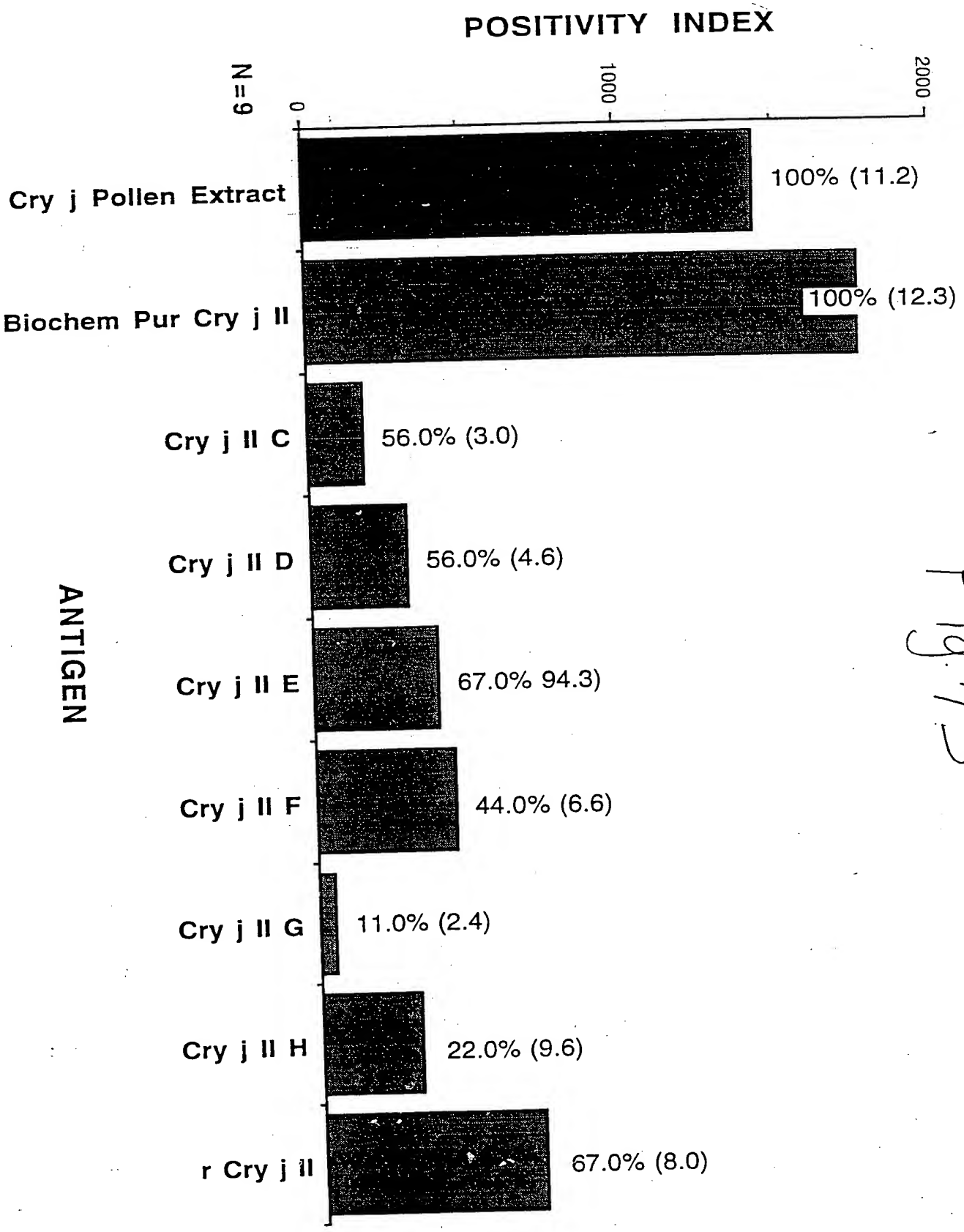

POSITIVITY INDEX
N=9
0
1000
2000
Cry j Pollen Extract
100% (11.2)
Biochem Pur Cry j II
100% (12.3)
Cry j II C
56.0% (3.0)
Cry j II D
56.0% (4.6)
Cry j II E
67.0% 94.3)
Cry j II F
44.0% (6.6)
Cry j II G
11.0% (2.4)
Cry j II H
22.0% (9.6)
r Cry j II
67.0% (8.0)
ANTIGEN

Fig. 43